

FILE 'BIOSIS, MEDLINE' ORDERED AT 09:43:27 ON 15 JAN 200

L1 12 S (FGF19)  
L2 9 DUP REM L1 (3 DUPLICATES REMOVED)  
L3 62308 S FUSION (W) (POLYPEPTIDE? OR PROTEIN? OR POLYPROTEIN?)  
L4 167774 S L3 OR IMMUNOCONJUGATE? OR CONJUGATE?  
L5 244 S L4 (P) SAPORIN?  
L6 33 S L5 (P) (FGF)  
L7 0 S L6 AND (MYELOMA? OR OSTEOSARCOMA?)  
L8 15 S ((FGF2) OR (FGF3)) (W) RECEPTOR?  
L9 70327 S (MYELOMA? OR OSTEOSARCOMA?)  
L10 0 S L8 (P) L9  
L11 13 S L8 AND CELL?  
L12 8 DUP REM L11 (5 DUPLICATES REMOVED)  
L13 17 DUP REM L6 (16 DUPLICATES REMOVED)  
L14 4 S L13 AND PROLIFERATION?

09/424,080



<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
JPAB,EPAB,DWPI,TDBD	l29 and (myeloma\$ or osteosarcoma\$)	0	<u>L30</u>
JPAB,EPAB,DWPI,TDBD	l26 same (FGF)	15	<u>L29</u>
JPAB,EPAB,DWPI,TDBD	l25 same l26	0	<u>L28</u>
JPAB,EPAB,DWPI,TDBD	l25 and l26	0	<u>L27</u>
JPAB,EPAB,DWPI,TDBD	l24 same saporin\$	28	<u>L26</u>
JPAB,EPAB,DWPI,TDBD	((FGF) adj (18)) or (FGF18)	2	<u>L25</u>
JPAB,EPAB,DWPI,TDBD	l23 or immunoconjugate\$ or conjugate\$	58618	<u>L24</u>
JPAB,EPAB,DWPI,TDBD	fusion adj (polypeptide\$ or protein\$ or polyprotein\$)	4035	<u>L23</u>
JPAB,EPAB,DWPI,TDBD	cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) adj receptor\$)	1	<u>L22</u>
USPT,PGPB	cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) adj receptor\$)	2	<u>L21</u>
USPT,PGPB	cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) same receptor\$)	5	<u>L20</u>
USPT,PGPB	cancer\$ same cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) same receptor\$)	1	<u>L19</u>
USPT,PGPB	l14 and (proliferation\$ or proliferate\$)	16	<u>L18</u>
USPT,PGPB	l14 and (proliferation\$ or proliferate\$)	16	<u>L17</u>
USPT,PGPB	l14 and proliferation\$ or proliferate\$	8330	<u>L16</u>
USPT,PGPB	l14 and myeloma and osteosarcoma and cells	0	<u>L15</u>
USPT,PGPB	l13 same (FGF)	16	<u>L14</u>
USPT,PGPB	l6 same saporin\$	109	<u>L13</u>
USPT,PGPB	l11 and saporin\$	0	<u>L12</u>
USPT,PGPB	l6 and l9	2	<u>L11</u>
USPT,PGPB	l6 same l9	0	<u>L10</u>
USPT,PGPB	l7 or l8	3	<u>L9</u>
USPT,PGPB	(FGF18)	1	<u>L8</u>
USPT,PGPB	(FGF) adj (18)	3	<u>L7</u>
USPT,PGPB	l5 or immunoconjugate\$ or conjugate\$	75647	<u>L6</u>
USPT,PGPB	fusion adj (polypeptide\$ or protein\$ or polyprotein\$)	12704	<u>L5</u>
USPT	(FGF18)	1	<u>L4</u>
USPT	(FGF-18) same saporin\$	0	<u>L3</u>
USPT	l1 or immunoconjugate\$ or conjugate\$	73088	<u>L2</u>
USPT	fusion adj (polypeptide\$ or protein\$ or polyprotein\$)	12092	<u>L1</u>





<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
JPAB,EPAB,DWPI,TDBD	cyclosporin\$ same (FK506) same rapamycin same interferon\$	2	<u>L20</u>
USPT,PGPB	cyclosporin\$ same (FK506) same rapamycin same interferon\$	12	<u>L19</u>
USPT,PGPB	117 and (inflammat\$ or cancer\$ or autoimmune\$ or disease\$ or disorder\$)	88	<u>L18</u>
USPT,PGPB	116 and composition\$	88	<u>L17</u>
USPT,PGPB	cyclosporin\$ and (FK506) and rapamycin and interferon\$	100	<u>L16</u>
USPT,PGPB	114 and composition\$	11	<u>L15</u>
USPT,PGPB	113 and (cancer\$ or lymphoma\$ or leukemia\$ or myeloma\$ or denocarcinoma\$ or autoimmune\$ or (chronic inflammatory disease\$) or (rheumatoid arthritis) or (myasthenia gravis) or (lupus erythematosus) or uveitis or (hyperproliferative disease\$) or (psoriasis vulgaris))	14	<u>L14</u>
USPT,PGPB	112 same interferon\$.clm.	21	<u>L13</u>
USPT,PGPB	cyclosporin\$ or (FK506) or rapamycin.clm.	4096	<u>L12</u>
USPT,PGPB	110 and composition.clm.	20	<u>L11</u>
USPT,PGPB	18 same 19	27	<u>L10</u>
USPT,PGPB	interferon\$.clm.	1623	<u>L9</u>
USPT,PGPB	immunosuppressant\$ or cyclosporin\$ or (FK506) or rapamycin.clm.	5361	<u>L8</u>
USPT,PGPB	11 same interferon\$	349	<u>L7</u>
USPT,PGPB	15 and 14	12	<u>L6</u>
USPT,PGPB	11 and composition\$	4653	<u>L5</u>
USPT,PGPB	(bioactive adj peptide\$) and interferon\$	143	<u>L4</u>
USPT,PGPB	(bioactive adj peptide\$) or interferon\$	12223	<u>L3</u>
USPT,PGPB	(bioactive adj peptide\$) and interferon\$	143	<u>L2</u>
USPT,PGPB	immunosuppressant\$ or cyclosporin\$ or (FK506) or rapamycin	5450	<u>L1</u>

09/424,080



=> s cyclosporin? (p) (FK506) (p) rapamycin  
L3 736 CYCLOSPORIN? (P) (FK506) (P) RAPAMYCIN

=> s interferon? (w) (alpha or beta or omega or tao)  
L4 46367 INTERFERON? (W) (ALPHA OR BETA OR OMEGA OR TAO)

=> s l3 and l4  
L5 3 L3 AND L4

=> dup rem l5  
PROCESSING COMPLETED FOR L5  
L6 3 DUP REM L5 (0 DUPLICATES REMOVED)



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:34:38 ; Search time 38.96 Seconds  
(without alignments)

15.210 Million cell updates/sec

Title: US-09-424-080A-1

Sequence: 1 LTKKYSR 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 50 summaries

Database :

A\_Geneseq\_1101.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:\*  
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:\*  
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:\*  
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:\*  
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:\*  
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:\*  
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:\*  
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:\*  
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:\*  
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	11	15	Interferon-recepto
2	42	100.0	18	15	Interferon-recepto
3	42	100.0	90	21	Partial human inte
4	42	100.0	133	3	Sequence encoded b
5	42	100.0	150	12	Interferon alpha 8
6	42	100.0	162	6	Sequence of hybrid
7	42	100.0	165	4	Thrl4, Met16 mutan
8	42	100.0	165	18	Human Interferon-a
9	42	100.0	165	18	Human Interferon-a
10	42	100.0	165	18	Human Interferon-a
11	42	100.0	165	18	Human Interferon-a

12	42	100.0	165	20	AAV43492
13	42	100.0	165	21	AAV82887
14	42	100.0	165	21	AAV44828
15	42	100.0	165	21	AAV44976
16	42	100.0	166	4	AAV30683
17	42	100.0	166	4	AAV30684
18	42	100.0	166	4	AAV30685
19	42	100.0	166	4	AAV30686
20	42	100.0	166	6	AAV50229
21	42	100.0	166	7	AAV60828
22	42	100.0	166	7	AAV60100
23	42	100.0	166	7	AAV60102
24	42	100.0	166	7	AAV60103
25	42	100.0	166	7	AAV60304
26	42	100.0	166	10	AAV90186
27	42	100.0	166	10	AAV90188
28	42	100.0	166	10	AAV90189
29	42	100.0	166	14	AAV42813
30	42	100.0	166	16	AAV67761
31	42	100.0	166	16	AAV67762
32	42	100.0	166	16	AAV43491
33	42	100.0	166	20	AAV05813
34	42	100.0	166	20	AAV05806
35	42	100.0	166	20	AAV05807
36	42	100.0	166	20	AAV05808
37	42	100.0	166	20	AAV05809
38	42	100.0	166	20	AAV05810
39	42	100.0	166	20	AAV05811
40	42	100.0	166	20	AAV05812
41	42	100.0	166	20	AAV05813
42	42	100.0	166	21	AAV07339
43	42	100.0	166	21	AAV07341
44	42	100.0	166	21	AAV07345
45	42	100.0	166	21	AAV07346
46	42	100.0	166	21	AAV07349
47	42	100.0	166	21	AAV28176
48	42	100.0	166	21	AAV28177
49	42	100.0	166	21	AAV28205
50	42	100.0	166	21	AAV82886

#### ALIGNMENTS

RESULT 1  
ID AAR47561 standard; peptide: 11 AA.  
AC AAR47561;  
XX  
DT 12-JUL-1994 (first entry)  
XX  
DE Interferon-receptor binding peptide #4.  
XX  
XX IFN $\gamma$  cell surface receptor; pharmaceutical carrier molecule;  
KW drug delivery; neoplastic tissue; infection;  
KW Type 1 human interferon receptor complex.  
XX  
OS Synthetic.  
XX  
XX WO9401457-A.  
XX  
XX PD 20-JAN-1994.  
XX  
XX PF 06-JUL-1993; 93WO-CA00279.  
XX  
XX PR 07-JUL-1992; 92US-0905739.  
XX  
XX PR 20-NOV-1992; 92US-0980525.  
XX  
XX PA (FISH/) FISH E N.  
XX  
XX PI Fish EN:  
XX

DR WPI: 1994-034987/04.

XX New interferon receptor-binding peptide(s) - useful for  
 PT delivering a pharmaceutically active drug to cells, e.g.  
 PT neoplastic, infected or inflamed tissue cells

PS Claim 4; Page 35; 51pp; English.

XX The critical clusters of amino acids in the different IFN- $\alpha$ s and  
 CC IFN- $\beta$  that interact with the Type 1 IFN receptor complex were  
 CC defined. These critical peptide domains were used to design  
 CC synthetic peptides AAR47562-R47564 that are useful as carriers for  
 CC pharmaceutical compositions.

XX Sequence 11 AA;

Query Match Best Local Similarity 100.0%; Score 42; DB 15; Length 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8

Db 2 ltekkysp 9

RESULT 2

AAR47562 standard; peptide; 18 AA.

XX AAR47562;

XX 12-JUL-1994 (first entry)

DE Interferon-receptor binding peptide #5.

KM IFN: cell surface receptor; pharmaceutical carrier molecule;

KM drug delivery; neoplastic tissue; infection;

XX Type 1 human interferon receptor complex.

OS Synthetic.

XX WO9401457-A.

XX 20-JAN-1994.

XX 06-JUL-1993; 93WO-CA00279.

XX 07-JUL-1992; 92US-0909739.

XX 20-NOV-1992; 92US-0980525.

XX (FISH) FISH E N.

XX Fish EN;

XX WPI: 1994-034987/04.

XX New interferon receptor-binding peptide(s) - useful for  
 PT delivering a pharmaceutically active drug to cells, e.g.  
 PT neoplastic, infected or inflamed tissue cells

PS Claim 5; Page 35; 51pp; English.

XX The critical clusters of amino acids in the different IFN- $\alpha$ s and  
 CC IFN- $\beta$  that interact with the Type 1 IFN receptor complex were  
 CC defined. These critical peptide domains were used to design  
 CC synthetic peptides AAR47562-R47564 that are useful as carriers for  
 CC pharmaceutical compositions.

XX Sequence 18 AA;

Query Match

100.0%; Score 42; DB 15; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8

Db 9 ltekkysp 16

RESULT 3

AAY55987 standard; Protein; 90 AA.

XX AAY55987;

XX 15-MAR-2000 (first entry)

DE Partial human interferon- $\alpha$ 5 protein.

KM Antiviral; anticancer; antiproliferative; human; interferon- $\alpha$ 5;

KM hepatic disease; hepatitis C; viral cirrhosis; hepatocellular carcinoma;

XX liver; gene expression.

OS Homo sapiens.

XX WO9598143-A1.

XX 18-NOV-1999.

XX 13-MAY-1999; 99WO-ES00134.

XX 13-MAY-1998; 98ES-0001003.

XX (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

XX Prieto Valtuena J, Civeira Murillo MP, Larrea Leoz E;

XX WPI: 2000-038959/03.

XX N-PSDB: AAZ47031.

XX Treating liver diseases with interferon- $\alpha$ 5 or nucleic acid encoding

XX it, particularly chronic hepatitis C -

XX Disclosure; Page 30; 36pp; Spanish.

XX This sequence corresponds to a fragment of the human interferon- $\alpha$ 5  
 CC protein (GenBank Accession No: X02956). The invention relates to a  
 CC method of using interferon- $\alpha$ 5 or its coding sequence to prepare  
 CC compositions for treatment of hepatic diseases, e.g. (i) chronic  
 CC hepatitis C; (ii) cirrhosis of viral origin and (iii) hepatocellular  
 CC carcinoma. The method restores the level of interferon- $\alpha$ 5, which  
 CC is reduced in diseased liver cells, to normal levels.

XX Sequence 90 AA;

Query Match Best Local Similarity 100.0%; Score 42; DB 21; Length 90;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8

Db 74 ltekkysp 81

RESULT 4

AAP20109 standard; Protein; 133 AA.

XX AAP20109;

XX 10-AUG-1992 (first entry)

DE Sequence encoded by leukocyte interferon LeIF G cDNA.

XX Viral infection; therapy; malignancy.  
 XX Homo sapiens.  
 XX GB2079291-A.  
 XX 20-JAN-1982.  
 XX 01-JUL-1981; 81GB-0120279.  
 XX 21-APR-1981; 81US-0256204.  
 XX 01-JUL-1980; 80US-0164986.  
 XX 08-SEP-1980; 80US-0184909.  
 XX 10-NOV-1980; 80US-0205578.  
 XX (HOFF) HOFFMANN-LA ROCHE AG.  
 XX (GENE-) GENENTECH INC.  
 XX Goeddel DVN, Pestka S;  
 XX WPI: 1982-04460E/03.  
 XX N-PSDB; AAN20096.  
 XX Mature human leukocyte interferon polypeptide(s) - prepd. from  
 XX microbes transformed with appropriate DNA sequences  
 XX Example; Fig 4; 20pp; English.  
 XX The inventors claim a polypeptide comprising the AA sequence of a  
 XX mature human Leif and a DNA sequence encoding it. Leif A-D, F, H-J  
 XX and encoding DNA are specifically claimed. They are natural allelic  
 XX variations. Leif is isolated from the leukocytes of humans with  
 XX chronic myelogenous leukaemia, induced to produce interferon with  
 XX Sendai or Newcastle disease virus; esp. the cell line KG-1.  
 XX Sequence 133 AA;  
 SQ

Query Match 100.0%; Score 42; DB 3; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEEKKISP 8  
 |||||  
 Db 98 ltekkysp 105

RESULT 5  
 AAR11799  
 AAR11799 standard; Protein; 150 AA.  
 AC AAR11799;  
 XX 03-JUN-1991 (first entry)  
 DT Interferon alpha 88 as CR2 ligand.  
 XX  
 DE Cellular receptor 2; CR2; binding site; BS; auto-immune disease;  
 KW Epstein-Barr Virus; EBV; B lymphocyte; ligand; interferon alpha 88.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Binding-site 72..86  
 FT Binding-site /note= "fragment pref. included"  
 FT Binding-site 75..82  
 FT /note= "fragment most pref. included"  
 XX WO9103251-A.  
 XX 21-MAR-1991.  
 XX

PF 04-SEP-1990; 90WO-US05027.  
 XX 20-APR-1990; 90US-0512118.  
 PR 08-SEP-1989; 89US-0404679.  
 XX  
 XX (CALB-) CALIF INST BIOLOGIC.  
 XX  
 XX Lernerhardt W;  
 XX WPI: 1991-101864/14.  
 XX  
 XX DNA segment encoding CR-2 ligand and CR2 binding site - used to  
 XX treat auto-immune disease, B-cell lymphoma and inhibit  
 XX Epstein-Barr virus infection  
 XX  
 XX Disclosure; Fig 2; 129pp; English.  
 XX  
 XX The ligand pref. includes the fragment indicated in the features.  
 XX The ligand pref. contains only a single BS and has an amino acid  
 XX sequence <100 (pref. <20) residues in length.  
 XX The ligand may also comprise a plurality of fragment 75..82.  
 XX A therapeutic compsn. contg. the polypeptide is used to stimulate  
 XX or inhibit B lymphocyte proliferation in patients with B cell  
 XX lymphoma. B lymphocytes and myeloma's can be stimulated in  
 XX patients with immunodeficiencies and immunoglobulin secretion by  
 XX hybridoma cultures can be boosted.  
 XX The compsn. can be administered to inhibit infection in vitro or in  
 XX vivo by Epstein-Barr Virus.  
 XX See also AAO1140-42 and AAR11355 for IFN alpha.  
 XX Sequence 150 AA;  
 SQ

Query Match 100.0%; Score 42; DB 12; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEEKKISP 8  
 |||||  
 Db 115 ltekkysp 122

RESULT 6  
 AAP50168  
 AAP50168 standard; Protein; 162 AA.  
 ID AAP50168;  
 AC AAP50168;  
 XX 30-OCT-1991 (first entry)  
 DT Sequence of hybrid alpha interferon (alpha-IFN).  
 XX  
 DE Antiviral agent; antitumour; interferon-alpha; virucide;  
 KW immunostimulant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI46903-A.  
 PD 03-JUL-1985.  
 PD 17-DEC-1984; 84EP-0115623.  
 PF 21-DEC-1983; 83US-0564066.  
 PR 19-DEC-1983; 83US-0562639.  
 XX  
 XX (SCHE) SCHERING CORP.  
 XX  
 XX Lebowitz PJ, Ryan MJ;  
 XX WPI: 1985-160612/27.  
 XX N-PSDB; AAN50236.  
 XX

PT New hybrid alpha-interferon with enhanced antiviral activity -  
PT prepd. by recombinant DNA procedures  
XX  
PS Claim 2; Page 22; 26pp; English.  
XX  
CC The hybrid alpha-IFN of the invention includes different portions of  
CC two different naturally occurring alpha-IFN as joined discrete sub-  
CC sequences. They are defined and arranged as a delta-4 alpha-2  
CC (Bgl II-1) sub-segment preceding a (Bgl II) alpha-1 segment. It has  
CC an antiviral activity of at least 100,000,000 units/mg by cytopathic  
CC effect-inhibition assay. Dose is 100,000 - 1000,000 units/square  
CC metre body surface daily topically. The N-terminal Met is optional.  
CC The claimed DNA sequence coding for the hybrid alpha-IFN may differ  
CC in accordance with the degeneracy of the genetic code.  
XX  
SQ Sequence 162 AA;

Query Match 100.0%; Score 42; DB 6; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKXSP 8  
DB 127 ltekxsp 134

CC Leukocyte interferon subtype F by two amino acid substitutions.  
CC It may be recombinantly produced in micro organisms transformed  
CC with the manufactured gene encoding it. See also AAP30673-P30686.  
XX  
SQ Sequence 165 AA;  
Query Match 100.0%; Score 42; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKXSP 8  
DB 131 ltekxsp 138

RESULT 8  
ID AAM43382 standard; protein; 165 AA.  
XX  
XX AAM43382;  
AC AAM43382;  
DE 07-APR-1998 (first entry)  
XX  
XX Human interferon-alpha 2b mutant (K132T).  
DE Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;  
KW nucleic acid binding agent; targeted expression; mutant.  
XX Homo sapiens.  
OS  
XX WO9733998-A1.  
XX 18-SEP-1997.  
XX  
XX 14-MAR-1997; 97WO-US03846.  
XX  
XX 14-MAR-1996; 96US-0616023.  
XX  
XX (IMMUNO-) IMMUNE RESPONSE CORP.  
XX  
XX Carlo DJ, Chlou HC;  
XX WPI; 1997-470878/43.

PT Delivering interferon gene to target mammalian cells in vivo or in  
PT vitro - as a molecular complex with a conjugate of nucleic acid  
PT binding agent and ligand for cell surface receptor, e.g. for  
PT treating virus infection or tumours  
XX  
XX Disclosure; Figure 11B; 52pp; English.  
XX  
XX This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
XX of mutant (K132T) which was recombinantly expressed in mice. A series  
XX of IFN-alpha 2b mutants were prepared with various single amino acid  
XX substitutions (AAM43382-90). The effect of these substitutions on  
XX antiviral activity (on mouse cells) for human IFN-alpha 2b was  
XX compared. This mutant had a relative activity of 0.1 compared with  
XX the native IFN-alpha 2b. The invention relates to a complex which  
XX targets expression of interferon in selected cells. The complex  
XX comprises the gene encoding interferon releasably linked to a conjugate  
XX of nucleic acid binding agent and a ligand which binds to a component on  
XX the surface of the cell. The method is used for targeted expression of  
XX recombinant IFN in selected cells, in vivo or in vitro, particularly for  
XX treatment of hepatitis, several forms of cancer and leukaemia and  
XX condyloma acuminatum, or for production of IFN for subsequent  
XX administration as exogenous protein.  
SQ Sequence 165 AA;

RESULT 7  
ID AAP30687 standard; Protein; 165 AA.  
XX  
XX AAP30687;  
AC AAP30687;  
DE 10-SEP-1992 (first entry)  
XX  
XX Thrl4, Met16 mutant human leukocyte interferon subtype F.  
XX  
XX Mutation; human; IFN.  
KW  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
XX FT 14  
XX FT /note= "mutation, Ala -> Thr"  
XX FT 16  
XX FT /note= "mutation, Ile -> Met"  
XX  
XX W08304053-A.  
XX  
XX 24-NOV-1983.  
XX  
XX 25-APR-1983; 83WO-US00605.  
XX  
XX 15-APR-1983; 83US-0483451.  
XX 06-MAY-1982; 82US-0375484.  
XX 12-DEC-1983; 83US-0560485.  
XX 21-SEP-1987; 87US-0099096.  
XX 01-JAN-1990; 90EP-0124236.  
XX  
XX (AMGE-) AMGEN INC.  
XX (AMGE-) AMGEN.  
XX (MOLE-) APPL MOLECULAR GENE.  
XX  
XX Alton NK, Peters MA, Stabinsky Y, Snilman DL;  
XX WPI; 1983-833208/48.  
XX  
XX Construction of large structural genes - useful in prepn. of  
XX human leukocyte interferon and analogues  
XX  
XX Claim 46; Page 85; 94pp; English.  
XX  
XX The sequence is that of a polypeptide which differs from human



Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYS 8  
 |||||  
 DB 130 ltkkysp 137

RESULT 9  
 AAM43386  
 ID AAM43386 standard; protein; 165 AA.  
 XX  
 AC AAM43386;  
 DT 07-APR-1998 (first entry)  
 DE Human interferon-alpha 2b mutant (Q125R; K132T).  
 XX  
 DE Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;  
 KW nucleic acid binding agent; targeted expression; mutant.  
 XX  
 XX Homo sapiens.  
 MO9733998-AL.  
 PD 18-SEP-1997.  
 PF 14-MAR-1997; 97WO-US03846.  
 XX  
 PR 14-MAR-1996; 96US-0616023.  
 PA (IMMU-) IMMUNE RESPONSE CORP.  
 PI Carlo DJ, Chlou HC;  
 PS WPI; 1997-470878/43.  
 DR  
 XX  
 XX Delivering interferon gene to target mammalian cells in vivo or in  
 PT vitro - as a molecular complex with a conjugate of nucleic acid  
 PT binding agent and ligand for cell surface receptor, e.g. for  
 PT treating virus infection or tumours  
 XX  
 PS Disclosure; Figure 11B; 52pp; English.  
 CC This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
 CC mutant (Q125R; K132T) which was recombinantly expressed in mice. A  
 CC series of IFN-alpha 2b mutants were prepared with various amino acid  
 CC substitutions (AAM43382-90). The effect of these substitutions on  
 CC antiviral activity (on mouse cells) for human IFN-alpha 2b was  
 CC compared. This mutant had a relative activity of 23 compared with  
 CC the native IFN-alpha 2b. The invention relates to a complex which  
 CC targets expression of interferon in selected cells. The complex  
 CC comprises the gene encoding interferon releasably linked to a conjugate  
 CC of nucleic acid binding agent and a ligand which binds to a component on  
 CC the surface of the cell. The method is used for targeted expression of  
 CC recombinant IFN in selected cells, in vivo or in vitro, particularly for  
 CC treatment of hepatitis, several forms of cancer and leukaemia and  
 CC condyloma acuminatum, or for production of IFN for subsequent  
 CC administration as exogenous protein.  
 CC  
 SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYS 8  
 |||||  
 DB 130 ltkkysp 137

RESULT 10  
 AAM43387

ID AAM43387 standard; protein; 165 AA.  
 XX  
 AC AAM43387;  
 DT 07-APR-1998 (first entry)  
 DE Human interferon-alpha 2b mutant (R121K; Q125R; K132T).  
 XX  
 DE Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;  
 KW nucleic acid binding agent; targeted expression; mutant.  
 XX  
 XX Homo sapiens.  
 MO9733998-AL.  
 PD 18-SEP-1997.  
 PF 14-MAR-1997; 97WO-US03846.  
 XX  
 PR 14-MAR-1996; 96US-0616023.  
 PA (IMMU-) IMMUNE RESPONSE CORP.  
 PI Carlo DJ, Chlou HC;  
 PS WPI; 1997-470878/43.  
 DR  
 XX  
 XX Delivering interferon gene to target mammalian cells in vivo or in  
 PT vitro - as a molecular complex with a conjugate of nucleic acid  
 PT binding agent and ligand for cell surface receptor, e.g. for  
 PT treating virus infection or tumours  
 XX  
 PS Disclosure; Figure 11B; 52pp; English.  
 CC This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
 CC mutant (R121K; Q125R; K132T) which was recombinantly expressed in mice.  
 CC A series of IFN-alpha 2b mutants were prepared with various amino acid  
 CC substitutions (AAM43382-90). The effect of these substitutions on  
 CC antiviral activity (on mouse cells) for human IFN-alpha 2b was  
 CC compared. This mutant had a relative activity of 170 compared with  
 CC the native IFN-alpha 2b. The invention relates to a complex which  
 CC targets expression of interferon in selected cells. The complex  
 CC comprises the gene encoding interferon releasably linked to a conjugate  
 CC of nucleic acid binding agent and a ligand which binds to a component on  
 CC the surface of the cell. The method is used for targeted expression of  
 CC recombinant IFN in selected cells, in vivo or in vitro, particularly for  
 CC treatment of hepatitis, several forms of cancer and leukaemia and  
 CC condyloma acuminatum, or for production of IFN for subsequent  
 CC administration as exogenous protein.  
 CC  
 SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYS 8  
 |||||  
 DB 130 ltkkysp 137

RESULT 11  
 AAM43390  
 ID AAM43390 standard; protein; 165 AA.  
 XX  
 AC AAM43390;  
 DT 07-APR-1998 (first entry)  
 DE Human interferon-alpha 2b mutant (Q125K; K132T).  
 XX  
 DE Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;  
 KW nucleic acid binding agent; targeted expression; mutant.

OY 1 LTKKYS 8  
 |||||  
 DB 130 ltkkysp 137

KW nucleic acid binding agent; targeted expression; mutant.  
 XX Homo sapiens.  
 OS  
 XX WO9733998-A1.  
 PN  
 XX 18-SEP-1997.  
 PD  
 XX 14-MAR-1997; 97WO-US03846.  
 PF  
 XX 14-MAR-1996; 96US-0616023.  
 PR  
 XX (IMMUNO) IMMUNE RESPONSE CORP.  
 PA  
 XX Carlo DJ, Chlou HC;  
 PI  
 XX WPI; 1997-470878/43.  
 DR  
 XX  
 PT Delivering interferon gene to target mammalian cells in vivo or in  
 PT vitro - as a molecular complex with a conjugate of nucleic acid  
 PT binding agent and ligand for cell surface receptor, e.g. for  
 PT treating virus infection or tumours  
 PS Disclosure; Figure 11B; 52pp; English.  
 XX  
 XX This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
 CC mutant (Q155K; K132T) which was recombinantly expressed in mice. A  
 CC series of IFN-alpha 2b mutants were prepared with various amino acid  
 CC substitutions (AAW43382-90). The effect of these substitutions on  
 CC antiviral activity (on mouse cells) for human IFN-alpha 2b was  
 CC compared. This mutant had a relative activity of 45 compared with  
 CC the native IFN-alpha 2b. The invention relates to a complex which  
 CC targets expression of interferon in selected cells. The complex  
 CC comprises the gene encoding interferon releasably linked to a conjugate  
 CC of nucleic acid binding agent and a ligand which binds to a component on  
 CC the surface of the cell. The method is used for targeted expression of  
 CC recombinant IFN in selected cells, in vivo or in vitro, particularly for  
 CC treatment of hepatitis, several forms of cancer and leukemia and  
 CC condyloma acuminatum, or for production of IFN for subsequent  
 CC administration as exogenous protein.  
 XX  
 XX Sequence 165 AA;  
 SQ  
 Query Match 100.0%; Score 42; DB 18; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTERKRYSP 8  
 |||||||  
 DB 130 ltekkySP 137  
 RESULT 12  
 AAY43492  
 ID AAY43492 standard; Protein; 165 AA.  
 XX  
 AC AAY43492;  
 XX  
 XX 26-JAN-2000 (first entry)  
 DT  
 XX A human interferon-alpha (IFN-alpha) protein.  
 DE  
 XX Interferon-alpha-2b; IFN-alpha; avb3 antagonist; avb3 receptor ligand;  
 KW metastasis-associated receptor ligand; angiogenesis; cell proliferation;  
 KW anti-angiogenic protein; avb3-integrin; cancer; arthritis;  
 KW macular degeneration; diabetic retinopathy; hemangioma; psoriasis;  
 KW osteoporosis; thrombosis; angina; atherosclerosis; antiviral;  
 KW antibacterial; antifungal.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO95f1638-A1.  
 PN

XX  
 PD 14-OCT-1999.  
 XX  
 XX 07-APR-1999; 99WO-US04295.  
 PF  
 XX 08-APR-1998; 98US-0081074.  
 PR  
 XX (SEAR) SEARLE & CO G D.  
 PA  
 XX Tjoeng FS, Fok KF;  
 PI  
 XX WPI; 1999-620196/53.  
 DR  
 XX  
 XX New conjugates of integrin antagonist and ligand for  
 PT metastasis-associated receptor, for treating angiogenesis-related  
 PT diseases, e.g. cancer  
 PS Claim 12; Page 102; 108pp; English.  
 XX  
 XX The present sequence represents an interferon-alpha (IFN-alpha) protein,  
 CC and can be conjugated to the avb3 antagonists of the invention. The  
 CC specification describes pharmaceutical compounds and their salts which  
 CC are dual avb3 receptor/metastasis-associated receptor ligands. These  
 CC compounds inhibit angiogenesis and thus proliferation of (cancer) cells.  
 CC One component binds to the avb3 receptor and the other to a  
 CC metastasis-associated receptor. The avb3 antagonists may also be  
 CC conjugated to anti-angiogenic proteins, such as IFN-alpha and its  
 CC derivatives. The compounds are used to treat angiogenesis-related  
 CC disorders (mediated by the avb3-integrin), specifically cancer (of lung,  
 CC breast, ovary, prostate, stomach, colon, kidney or bladder, also  
 CC melanoma, hepatoma, sarcoma and lymphoma), arthritis and macular  
 CC degeneration, and also diabetic retinopathy, hemangioma, psoriasis,  
 CC osteoporosis, thrombosis, angina, atherosclerosis etc. The compounds may  
 CC also be useful as antiviral, antibacterial and antifungal agents.  
 XX  
 XX Sequence 165 AA;  
 SQ  
 Query Match 100.0%; Score 42; DB 20; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTERKRYSP 8  
 |||||||  
 DB 130 ltekkySP 137  
 RESULT 13  
 AAY82887  
 ID AAY82887 standard; Protein; 165 AA.  
 XX  
 AC AAY82887;  
 XX  
 XX 25-JUL-2000 (first entry)  
 DT  
 XX N-terminal modified interferon alpha A/D hybrid.  
 DE  
 XX Biconjugate: a.vb\_3 integrin; interferon alpha; angiogenesis;  
 KW cancer; tumour; osteoporosis; Paget's disease; Karpov's sarcoma;  
 KW periodontal disease; metastasis; neoplasia; retinopathy; arthritis;  
 KW psoriasis; leukemia; malignant melanoma; atherosclerosis;  
 KW smooth muscle cell migration; inhibition; treatment; antagonist;  
 KW angina; thrombosis; restenosis; antiviral; antifungal;  
 KW antibacterial.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200009143-A1.  
 PN  
 XX 24-FEB-2000.  
 PD  
 XX 07-APR-1999; 99WO-US04296.  
 PF  
 XX



FT	Region	96..166
FT	/note= "Derived from IFN-alpha2a"	
XX		
FN	WO200006596-A2.	
PD	10-FEB-2000.	
XX		
XX	29-JUN-1999;	99WO-US14749.
PF	28-JUL-1998;	98US-0094407.
PR	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	
XX		
PA	Zoon KC, Hu R, Bekisz JB, Hayes MP:	
PI		
XX	WPI; 2000-195259/17.	
DR	N-PDSB; AAZ50512.	
XX		
Pt	Novel human hybrid interferons and their mutants, useful for treating	
Pt	viral infections such as rabies and hepatitis B and C, and cancers such	
PT	as melanoma, multiple myeloma, and papilloma -	
PS	Claim 10; Page 49-50; 66pp; English.	
XX		
CC	The present amino acid sequence is the human hybrid interferon-alpha	
CC	(HuIFNalpha) polypeptide Hy-3, comprising a fusion of IFN-alpha2a and	
CC	IFN-alpha2c. This hybrid IFN has antiviral, antiproliferative,	
CC	cytostatic and immunomodulator activity. Hy-3 exhibited a higher	
CC	antiproliferative activity than the parental interferons, IFN-alpha2c	
CC	and IFN-alpha2a and other IFN-alpha hybrids.	
CC	Hybrid IFNs are used for treatment of viral diseases, such as	
CC	encephalomyocarditis, influenza, respiratory tract infections, rabies,	
CC	vital zoonoses, arbovirus, Herpes simplex and Varicella zoster	
CC	infections, keratitis, acute haemorrhagic conjunctivitis and hepatitis B	
CC	and C. It is also used for modulation of immune system, regulation of	
CC	tumour growth and cancers such as osteogenic sarcoma, multiple myeloma,	
CC	Hodgkin's disease, nodular, poorly differentiated lymphoma, acute	
CC	lymphocytic leukaemia, acute myeloid leukaemia, breast carcinoma,	
CC	melanoma, papilloma and nasopharyngeal carcinoma in humans.	
SQ	Sequence 165 AA;	
	Query Match 100.0%; Score 42; DB 21; Length 165;	
	Best Local Similarity 100.0%; Pred. No. 1.3;	
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DY	1 ILEKRYSP 8	
DB		
	130 ILEKRYSP 137	
RESULT 16		
AAP30683		
ID AAP30683 standard; Protein: 166 AA.		
AC AAP30683;		
DT 10-SEP-1992 (first entry)		
DE Synthetic human leukocyte interferon subtype F.		
XX Mutation; human; IFN.		
OS Synthetic.		
PN WO8304053-A.		
PD 24-NOV-1983.		
PE 25-APR-1983; 83WO-US00605.		
PR 15-APR-1983; 83US-0483451.		

```
PR      06-MAY-1982;      82US-0375494.  
PR      12-DEC-1983;      83US-0560495.  
PR      21-SEP-1987;      87US-0099096.  
XX      01-JAN-1990;      90EP-0124236.  
  
PA      (AMGE-) AMGEN INC.  
PA      (AMGE-) AMGEN  
PA      (MOLE-) APPL MOLECULAR GENE.  
PI      Alton NK, Peters MA, Stabinsky Y, Sultman DL;  
XX  
DR      WPI: 1983-833208/48.  
DR      N-PSDB; AAN30318.  
XX  
PT      Construction of large structural genes - useful in prepn. of  
PT      human leukocyte interferon and analogues  
XX  
PS      Claim 42; Page 84; 94pp; English.  
XX  
CC      The sequence is that of human leukocyte interferon subtype F,  
CC      encoded by a gene manufactured such that it is capable of directing  
CC      synthesis of the interferon in a selected host microorganism.  
CC      See also AAP30673-P30687.  
XX  
SQ      Sequence      166 AA;  
  
Query Match      100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity      100.0%; Pred. No. 1.3;  
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0.  
  
OY      1 LTERKRYSP 8  
        |||||||  
Db       131 ltekkysp 138  
  
RESULT 17  
AAP30684 ID AAP30684 standard; Protein; 166 AA.  
XX  
AC AAP30684;  
XX  
XX      10-SEP-1992 (first entry)  
DE XX  
DE XX Consensus human leukocyte interferon #1.  
XX  
KW Mutation; human; IFN.  
XX  
OS Synthetic.  
OS XX  
XX  
FH Key Location/Qualifiers  
FH      22  
FT Region /note= "mutation, Gly -> Arg"  
FT      76  
FT Region /note= "mutation, Thr -> Ala"  
FT      78  
FT Region /note= "mutation, Glu -> Asp"  
FT      79  
FT Region /note= "mutation, Gln -> Glu"  
FT      86  
FT Region /note= "mutation, Ser -> Tyr"  
FT      90  
FT Region /note= "mutation, Asn -> Tyr"  
FT      96  
FT Region /note= "mutation, Met -> Leu"  
FT      156  
FT Region /note= "mutation, Lys -> Thr"  
FT      157  
FT Region /note= "mutation, Ile -> Asn"  
FT      158  
FT Region /note= "mutation, Phe -> Leu"  
XX
```

XX 24-NOV-1983.  
PD  
XX  
XX 25-APR-1983; 83WO-US00605.  
PF  
XX 15-APR-1983; 83US-0483451.  
PR 06-MAY-1982; 82US-0375494.  
PR 12-DEC-1983; 83US-0560495.  
PR 21-SEP-1987; 87US-009096.  
PR 01-JAN-1990; 90EP-0124236.  
XX  
XX (AMGE-) AMGEN INC.  
PA (AMGE-) AMGEN.  
PA (MOLE-) APPL MOLECULAR GENE.  
XX  
XX Alton NK, Peters MA, Stabinsky Y, Sultman DL;  
PI  
XX WPI: 1983-833208/48.  
DR  
XX  
XX Construction of large structural genes - useful in prepn. of  
PT human leukocyte interferon and analogues  
XX  
XX Claim 38; Page 84; 94pp; English.  
CC The sequence is that of a consensus human leukocyte interferon,  
CC encoded by a gene manufactured such that it is capable of directing  
CC synthesis of the interferon in a selected host microorganism.  
CC See also AAP30673-P30687.  
XX  
XX Sequence 166 AA;  
SQ  
Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTKKXSP 8  
DB 131 ltkkxsp 138  
RESULT 18  
AAP30685  
ID AAP30685 standard; Protein; 166 AA.  
XX  
XX AAP30685;  
AC  
XX  
DT 10-SEP-1992 (first entry)  
XX  
XX Consensus human leukocyte interferon #2.  
KM Mutation; human; IFN.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH 14  
FT Region /note= "mutation, Ala -> Thr"  
FT 16  
FT Region /note= "mutation, Ile -> Met"  
FT 22  
FT Region /note= "mutation, Gly -> Arg"  
FT 76  
FT Region /note= "mutation, Thr -> Ala"  
FT 78  
FT Region /note= "mutation, Glu -> Asp"  
FT 79  
FT Region /note= "mutation, Gln -> Glu"  
FT 86  
FT Region /note= "mutation, Ser -> Tyr"  
FT 90  
FT Region /note= "mutation, Asn -> Tyr"  
FT 96  
FT Region

FT Region /note= "mutation, Met -> Leu"  
FT 156  
FT Region /note= "mutation, Lys -> Thr"  
FT 157  
FT Region /note= "mutation, Ile -> Asn"  
FT 158  
FT Region /note= "mutation, Phe -> Leu"  
XX  
XX W08304053-A.  
XX  
XX 24-NOV-1983.  
PD  
XX  
XX 25-APR-1983; 83WO-US00605.  
PF  
XX  
XX 15-APR-1983; 83US-0483451.  
PR 06-MAY-1982; 82US-0375494.  
PR 12-DEC-1983; 83US-0560495.  
PR 21-SEP-1987; 87US-009096.  
PR 01-JAN-1990; 90EP-0124236.  
XX  
XX (AMGE-) AMGEN INC.  
PA (AMGE-) AMGEN.  
PA (MOLE-) APPL MOLECULAR GENE.  
XX  
XX Alton NK, Peters MA, Stabinsky Y, Sultman DL;  
PI  
XX WPI: 1983-833208/48.  
DR  
XX  
XX Construction of large structural genes - useful in prepn. of  
PT human leukocyte interferon and analogues  
XX  
XX Claim 38; Page 84; 94pp; English.  
PS  
XX  
XX The sequence is that of a consensus human leukocyte interferon,  
CC encoded by a gene manufactured such that it is capable of directing  
CC synthesis of the interferon in a selected host microorganism.  
CC See also AAP30673-P30687.  
XX  
XX Sequence 166 AA;  
SQ  
Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTKKXSP 8  
DB 131 ltkkxsp 138  
RESULT 19  
AAP30686  
ID AAP30686 standard; Protein; 166 AA.  
XX  
XX AAP30686;  
AC  
XX  
DT 10-SEP-1992 (first entry)  
XX  
XX Consensus human leukocyte interferon #3.  
KM Mutation; human; IFN.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH 22  
FT Region /note= "mutation, Gly -> Arg"  
FT 76  
FT Region /note= "mutation, Thr -> Ala"  
FT 78  
FT Region /note= "mutation, Glu -> Asp"  
FT 79  
FT Region /note= "mutation, Gln -> Glu"  
FT

```

FT Region 86
FT /note= "mutation, Ser -> Tyr"
FT 90
FT /note= "mutation, Asn -> Tyr"
FT 96
FT /note= "mutation, Met -> Leu"
FT 114
FT /note= "mutation, Asn -> Tyr"
FT 121
FT /note= "mutation, Met -> Leu"
FT 156
FT /note= "mutation, Lys -> Thr"
FT 157
FT /note= "mutation, Ile -> Asn"
FT 158
FT /note= "mutation, phe -> Leu"
FT Region

XX W08304053-A.
XX 24-NOV-1983.
XX
XX
XX 25-APR-1983; 83WO-US00605.
XX
XX 15-APR-1983; 83US-0483451.
XX 06-MAY-1982; 82US-0375494.
XX 12-DEC-1983; 83US-0560495.
XX 21-SEP-1987; 87US-0099096.
XX 01-JAN-1990; 90EP-0124236.
XX
XX (AMGE-) AMGEN INC.
XX (AMGE-) AMGEN.
XX (MOLE-) APPL MOLECULAR GENE.
XX
XX Alton NK, Peters MA, Stabinsky Y, Sultman DL;
XX WPI: 1983-833208/48.
XX
XX Construction of large structural genes - useful in prepn. of
XX human leukocyte interferon and analogues
XX
XX Claim 38; Page 84; 94pp; English.
XX
XX The sequence is that of a consensus human leukocyte interferon,
XX encoded by a gene manufactured such that it is capable of directing
XX synthesis of the interferon in a selected host microorganism.
XX See also AAP30673-P30687.
XX
XX Sequence 166 AA;
XX
XX
XX Query Match 100.0%; Score 42; DB 4; Length 166;
XX Best Local Similarity 100.0%; Pred. No. 1.3;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LTERKYP 8
DB 131 lterkyp 138

RESULT 20
AAP50229
ID AAP50229 standard; Protein; 166 AA.
XX
XX AAP50229;
XX
XX 24-NOV-1991 (first entry)
XX
XX Interferon alpha-1.
XX
XX Interferon alpha-1; hybrid protein; crossover region.
XX
XX Key Location/Qualifiers
XX Region 63..66

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FT Region /label= crossover region A
FT 88..95
FT /label= crossover region B
FT 88..101
FT /label= crossover region C
FT 88..106
FT /label= crossover region D
FT 109..113
FT /label= crossover region E
FT 114..117
FT /label= crossover region F
FT 126..131
FT /label= crossover region G
FT 133..151
FT /label= crossover region H
FT 153..154
FT /label= crossover region I
FT 155..161
FT /label= crossover region J
FT Region

XX EP141484-A.
XX
XX 15-MAY-1985.
XX
XX 05-JUN-1984; 84EP-0303787.
XX
XX 10-JUN-1983; 83GB-0015980.
XX
XX (BIOJ ) BIOGEN NV.
XX
XX Weissmann C, Weber H;
XX
XX WPI: 1985-117654/20.
XX N-PSDB; AAN50273.
XX
XX New hybrid DNA sequences and hybrid polypeptide(s) - useful in prodn.
XX of interferon(s), lymphokines, viral antigens, etc.
XX
XX Disclosure; Fig. 6A-C; 47pp; English.
XX
XX The DNA encoding Interferon alpha-1 may be fused to a second
XX coding sequence, eg for animal or human alpha, beta or gamma-
XX interferons, lymphokines, foot-and-mouth disease antigens, to form a
XX hybrid DNA. The DNA must be fused to the second DNA sequence in the
XX same reading frame to maintain a constant reading frame through a
XX crossover region common to both sequences. The hybrid sequences are
XX obt'd. without the need for chance availability of restriction sites
XX to be combined. Sequential deletions to give prods. with modified
XX properties, activity and specificity are reliable.
XX
XX Sequence 166 AA;
XX
XX
XX Query Match 100.0%; Score 42; DB 6; Length 166;
XX Best Local Similarity 100.0%; Pred. No. 1.3;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LTERKYP 8
DB 131 lterkyp 138

RESULT 21
AAP60828
ID AAP60828 standard; Protein; 166 AA.
XX
XX AAP60828;
XX
XX 26-JUL-1991 (first entry)
XX
XX Sequence of interferon-alpha 1.
XX
XX Hepatitis B therapy; Kerato-conjunctivitis epidemica;
XX

```



OY 1 LTKKXSP 8  
 |||||  
 DB 131 ltkkxsp 138

## RESULT 24

AAP60103  
 ID AAP60103 standard; Protein; 166 AA.

XX  
 AC AAP60103;

XX 07-AUG-1991 (first entry)

DE Sequence of hybrid human lymphoblastoid interferons (LYIFN) alpha-2  
 and alpha-3, B1D2D3D4.

XX Antiviral agent; neoplastic agent; therapy.

XX Homo sapiens.

XX EP205404-A.

XX 17-DEC-1986.

XX 05-JUN-1986; 86EP-0810243.

XX 11-JUN-1985; 85GB-0014726.

XX (CIBA ) CIBA GEIGY AG.

XX Meyer F, Hinnen A, Meister A, Grutter MK, Alkan S;

XX WPI; 1986-333879/51.

XX New hybrid lymphoblastoid interferon(s) - useful as antiviral and  
 neoplastic agents.

XX Claim 6; Page 73; 82pp; English.

XX The hybrid polypeptides of the invention have an AA sequence composed  
 of 2-4 sub-sequences corresp. in AA identity and number to sub-  
 sequences of LYIFN-alpha-2 and LYIFN-alpha-3. In particular, the  
 claimed polypeptides have the AA sequence of : (i) AAs 1-150 of  
 -alpha-2 and 151-166 of -alpha-3; (ii) AAs 1-92 of -alpha-2, 93-150  
 of -alpha-3 and 151-166 of -alpha-2 or (iii) AAs 1-60 of -alpha-2,  
 61-92 of -alpha-3, 93-150 of -alpha-2 or -alpha-3 and 151-166 of  
 -alpha-2 or -alpha-3. AAP60099-P60104 are specifically claimed.

XX Sequence 166 AA;

Query Match 100.0%; Score 42; DB 7; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKXSP 8  
 |||||

DB 131 ltkkxsp 138

## RESULT 25

AAP60304  
 ID AAP60304 standard; Protein; 166 AA.

XX  
 AC AAP60304;

XX 23-AUG-1991 (first entry)

DE Sequence of interferon (IFN) alpha S51B10.

XX Antiviral; antitumour.

XX

OS Homo sapiens.

XX EPI73887-A.

XX 12-MAR-1986.

XX 10-AUG-1985; 85EP-0110061.

XX 27-AUG-1984; 84JP-0179105.

XX (SHIO ) SHIONOGI KK.

XX Teraoka H, Sato K, Tanaka K;

XX WPI; 1986-070431/11.

XX N-PSDB; AAN60236.

XX New interferon alpha S51B10 and alpha S17H9 - prepd. by DNA  
 recombinant techniques

XX Claim 1; Fig 2; 37pp; English.

XX IFN alpha-S51B10 and IFN alpha-S17H9 have antiviral and antitumour  
 CC activities. Dosage is 1,000,000 - 10,000,000 units per day. IFNs are  
 CC prepared from Ball-1 cells induced with Sendai virus by known  
 CC recombinant DNA techniques.

XX Sequence 166 AA;

Query Match 100.0%; Score 42; DB 7; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKXSP 8  
 |||||

DB 131 ltkkxsp 138

Search completed: January 15, 2002, 08:40:02  
 Job time: 324 sec



Script started on Tue Jan 15 10:27:05 2002

stic10% m plr.find  
! FINDPATTERNS on plr: \* allowing 0 mismatches

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)(P,R,D,L)

OXCKP2 ck: 4180 len: 724 ! acyl-CoA oxidase (EC 1.3.3.6) PXP2, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSRHSL

250: TFIVP

OXCKX4 ck: 4824 len: 709 ! acyl-CoA oxidase (EC 1.3.3.6) POX4, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

228: TFVVP

OXCKAX ck: 6643 len: 502 ! acyl-CoA oxidase (EC 1.3.3.6) POX4-2, perox

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

21: TFVVP

OXCKX ck: 2978 len: 709 ! acyl-CoA oxidase (EC 1.3.3.6) AOX, peroxisc

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

228: TFVVP

OXCKPM ck: 8367 len: 709 ! acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

228: TFVVP

OXCKX5 ck: 3893 len: 662 ! acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

213: TFVVP

S66044 ck: 714 len: 217 ! deoxypurine kinase (EC 2.7.1.-) yaaF - Bac

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRIDYDL

186: CPVLK

A64107 ck: 3967 len: 366 ! DNA-directed DNA polymerase (EC 2.7.7.7) IT

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(Q)(T)(E)(D)(Y)(R)(L)  
LQIEDYRL

35: LNNVL

RRNZ2 ck: 6550 len: 2,165 ! genome polyprotein - human respiratory sync

[7m-More--(2%)] m [stic10%

stic10%

stic10% tail plrfind

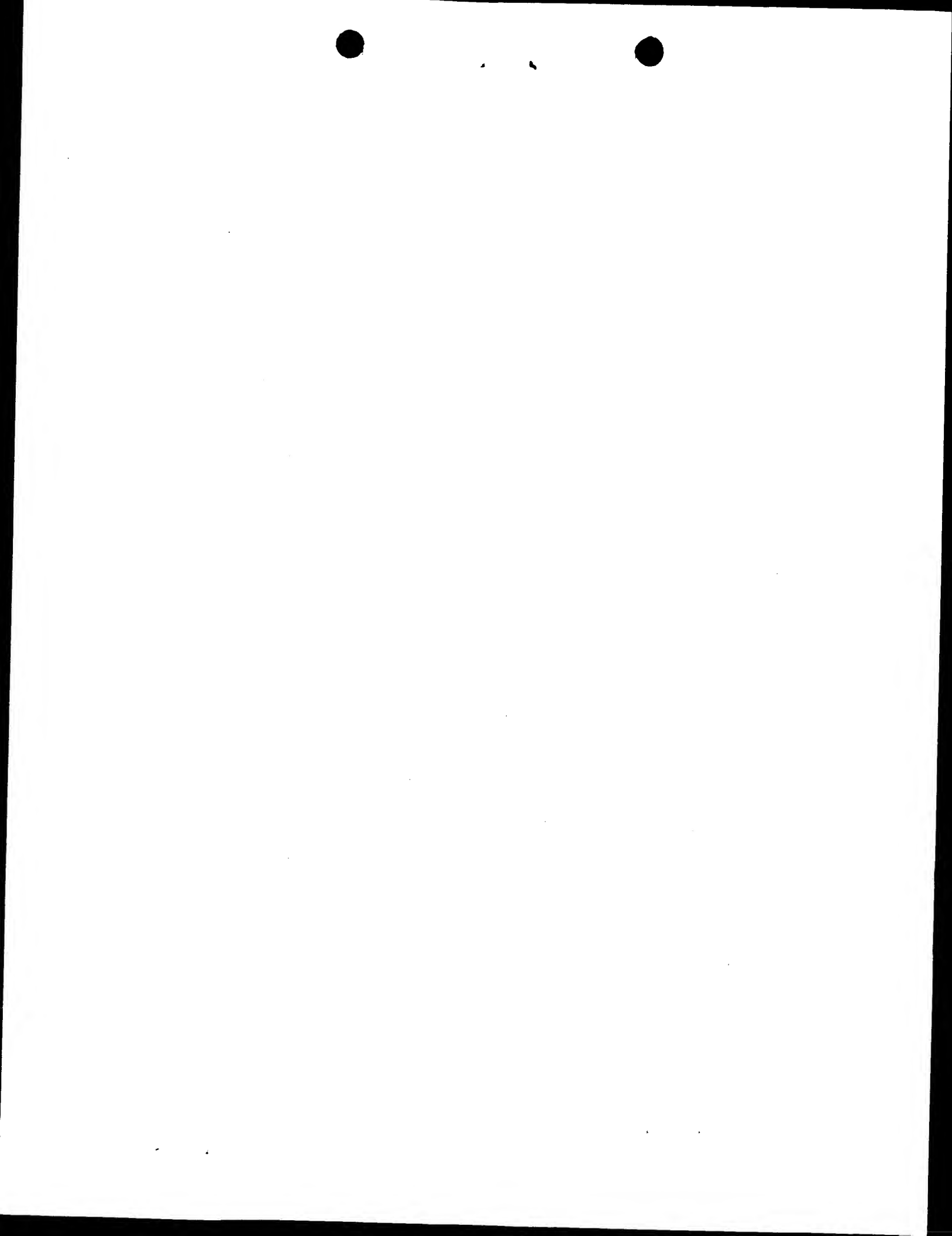
.find

Databases searched:

NBRF, Release 68.0, Released on 31Mar2001, Formatted on 26Jun2001

Total finds: 344  
Total length: 76,174,552  
Total sequences: 219,241  
CPU time: 04:37.90

Script done on Tue Jan 15 10:27:24 2002



Script started on Tue Jan 15 10:31:55 2002

stic10% m swp.find

! FINDPATTERNS on swp: \* allowing 0 mismatches

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)(P,R,D,L)

ACTR\_CAVPO ck: 5058 len: 297 1 Q92159 cavia porcellus (guinea pig) . adrenc

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(M)(A)(R)(S)(H)(A)(R)  
LMARSHAR

198: YVHMF

AIDA\_ECOLI ck: 8339 len: 1,286 1 Q03155 escherichia coli . adhesin aida-i pre

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(E)(E)(K)(Y)(N)(L)  
LEEKYNL

1,118: VKGCG

AMY\_BUTFI ck: 4687 len: 976 1 P30269 butyrivibrio fibrisolvens . alpha-amy

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(M)(I)(E)(R)(Y)(N)(D)  
LMIERYND

540: GNIOT

APE2\_AERPE ck: 3114 len: 167 1 O73943 aeropyrum pernix . homing endonuclease

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(T)(R)(M)(K)(Y)(R)(R)  
LTRMKYRR

112: EIVLT

ASO\_CUCPEM ck: 1447 len: 552 1 P37064 cucurbita pepo var. melopepo (zucchini)

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(G)(A)(M)(K)(Y)(N)(L)  
LGAMKYNL

377: PPTPY

BIOB\_SCHPO ck: 8853 len: 363 1 O59778 schizosaccharomyces pombe (fission Y)

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(G)(E)(K)(H)(D)(R)  
LGEKKHDR

213: GGILG

BUD6\_YEAST ck: 5257 len: 788 1 P41697 saccharomyces cerevisiae (baker's ye

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(E)(A)(N)(K)(H)(D)(L)  
LEANKHDL

489: LPQPG

CADE\_DROME ck: 2829 len: 1,507 1 Q24298 drosophila melanogaster (fruit fly)

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(Q)(A)(N)(D)(Y)(D)(D)  
LQANDIDD

753: GHVVO

CAOI\_CANFR ck: 2901 len: 661 1 P08790 candida tropicalis (yeast) . acyl-coe

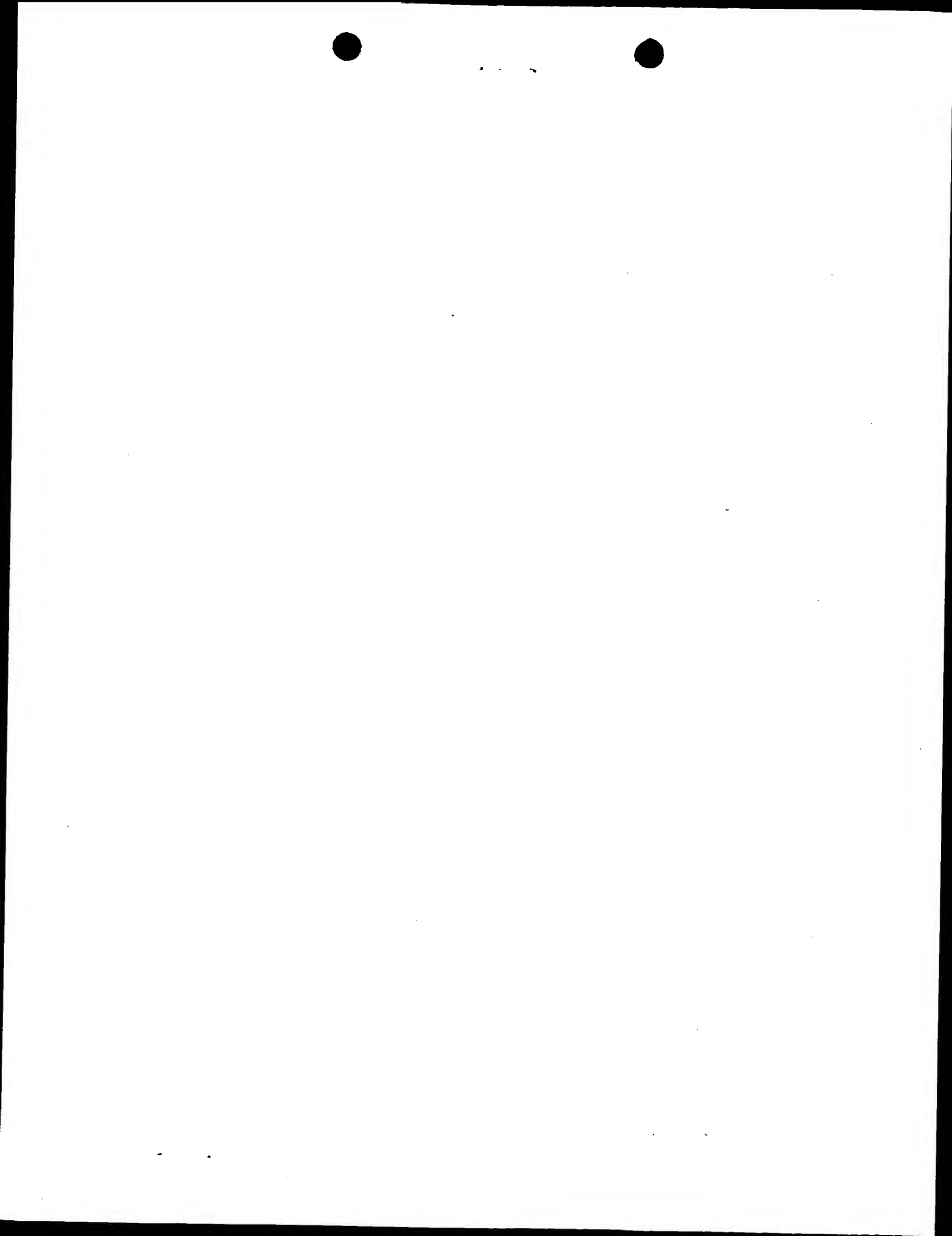
1 [7m--more--(1%)] m [kstic10%  
stic10%  
stic10%  
stic10% tail swp.find

Databases searched:

SWISS-PROT, Release 39.2, Released on 24Aug2001, Formatted on 27Aug2001  
SPTREMBL, Release 17.0, Released on 1Jun2001, Formatted on 26Jun2001

Total finds: 654  
Total length: 182,937,156  
Total sequences: 573,564  
CPU time: 11:27.72

stic10%  
script done on Tue Jan 15 10:32:11 2002



Script started on Tue Jan 15 10:33:38 2002  
stic10% m agen.res

> 0 <  
01 10 Intelligences  
> 0 <

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "agen" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence: "09-424080.key";

Selected sequence key from "seq2 AA preliminary pattern

seq2 (AA) ID seq2 AA preliminary pattern  
1 followed by  
2 1  
2 t or r or g or m or e or g  
2 e or r or d or l or i or a  
2 k or r or n or m or s or e  
2 k or r or d or n or s  
2 y or h  
2 s or r or d or n or a  
2 p or r or d or l

Selected data banks and files:

Data bank : A-Geneseq 35.2, all entries

-- Output Parameters --

Format Options:	File Options:
Nucleic acid code matching	Exact
Find non-matching hits only	No
Report key used	Yes
Note position of hit	Yes
Display full annotations	Yes
Sequence context	25

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

P90186 : Hybrid alpha-interferon.

(from "A-Geneseq 35.2")

P90186 standard; peptide: 166 AA.

AC P90186;

DE 14-DEC-1989 (first entry)

DT Hybrid alpha-interferon.

KW Hybrid; alpha-interferon; alpha-D gene; alpha-B gene; muramylpeptide;

KW human; synthetic; herpes simplex virus 1 and 2; tumours; Lewis lung

KW carcinoma; B16-B16 melanoma; synergistic.

OS Synthetic.

FH Key

FT region

FT region

FT region

FT region

FT region

FT region

FT region

FT region

FT region

FT region

FT region

FT region

FT region

FT region

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FT region

FT region

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FT region

FT region

FT region

FT region

CC Hybrid alpha-interferon consisting of 4 fragments of human  
CC lymphoblastoid or leukocyte interferons-alpha-B and -alpha-D. This is  
CC hybrid B16D3B4 which correspond, in order, to the regions specified  
CC starting with B1 (amino acids 1-60 of interferon-alpha-B). The hybrids  
CC (P90185-90) act synergistically, in a compsn. with muramyl peptide, to  
CC treat virus infections in human and veterinary medicine esp. herpes  
CC simplex virus 1 and 2. They also reduce development of metastases from  
CC some tumours, eg B16-B16 melanoma or Lewis lung carcinoma.  
SO Sequence 166 AA:  
SQ 11 A: 11 R: 5 N: 11 D: 0 B: 4 C: 12 Q: 15 E: 0 Z: 2 G: 3 H:  
SQ 9 I: 21 L: 11 K: 5 M: 10 F: 5 P: 13 S: 7 T: 1 W: 4 Y: 6 V:  
Found using 'seq2' (09-424080.key)

106 vgetplmadslavkkyfrirtilyltekkyspcawevvraeimsfsislnlqrlk  
131 138

-----  
1 match found in sequence:  
P90188 : Hybrid alpha-interferon.  
(from "A-Geneseq 35.2")  
ID P90188 standard; peptide: 166 AA.  
AC P90188;  
DE 14-DEC-1989 (first entry)  
DT Hybrid alpha-interferon.  
KW Hybrid; alpha-interferon; alpha-D gene; alpha-B gene; muramylpeptide;  
KW human; synthetic; herpes simplex virus 1 and 2; tumours; Lewis lung  
KW carcinoma; B16-B16 melanoma; synergistic.  
OS Synthetic.  
FH Key

Location/Qualifiers
FT region 1..60
FT region 61..92
FT region 93..150
FT region 151..166

PN EP-329609-A.  
PD 23-AUG-1989.  
PE 06-FEB-1989; GB-003365.  
PR 13-FEB-1988; GB-003365.  
PA (CIBA) Ciba Geigy AG.  
PI Gangemi JD, Hochkeppel HK;  
PI WPI: 89-243490/34.  
DR Synergistic antiviral compsn. - contg. hybrid alpha interferon  
PT and muramyl peptide esp. active against herpes simplex.  
PS Disclosure: page 2; 13pp; English.

CC Hybrid alpha-interferon consisting of 4 fragments of human  
CC lymphoblastoid or leukocyte interferons-alpha-B and -alpha-D. This is  
CC hybrid B16D3B4 which correspond, in order, to the regions specified  
CC starting with B1 (amino acids 1-60 of interferon-alpha-B). The hybrids  
CC (P90185-90) act synergistically, in a compsn. with muramyl peptide, to  
CC treat virus infections in human and veterinary medicine esp. herpes  
CC simplex virus 1 and 2. They also reduce development of metastases from  
CC some tumours, eg B16-B16 melanoma or Lewis lung carcinoma.  
SO Sequence 166 AA:  
SQ 11 A: 11 R: 5 N: 11 D: 0 B: 4 C: 12 Q: 15 E: 0 Z: 2 G: 3 H:  
SQ 9 I: 20 L: 12 K: 5 M: 10 F: 5 P: 12 S: 7 T: 2 W: 4 Y: 6 V:  
Found using 'seq2' (09-424080.key)

106 vgetplmadslavkkyfrirtilyltekkyspcawevvraeimsfsislnlqrlk  
131 138

-----  
1 match found in sequence:  
P90189 : Hybrid alpha-interferon.  
(from "A-Geneseq 35.2")

ID P90189 standard; peptide; 166 AA.  
 AC P90189;  
 DT 14-DEC-1989 (first entry)  
 DE Hybrid alpha-interferon.  
 KW human; synthetic; herpes simplex virus 1 and 2; tumours; Lewis lung carcinoma; B16-B16 melanoma; synergistic.  
 OS Synthetic.  
 FH Key  
 FT region 1..60  
 FT region 61..92  
 FT region 93..150  
 FT region 151..166  
 PN EP-329609-A.  
 PD 23-AUG-1989.  
 PF 06-FEB-1989; 810100.  
 PR 13-FEB-1988; GR-003365.  
 PA (CIBA) Ciba Geigy AG.  
 PI Gangeml JD, Hockheppel HK;  
 DR WPI: 89-243490/34.  
 PT Synergistic antiviral compn. - contg. hybrid alpha interferon  
 PS and muramyl peptide esp. active against herpes simplex.  
 PS Disclosure; page 3; 13pp; English.  
 CC Hybrid alpha-interferon consisting of 4 fragments of human  
 CC lymphoblastoid or leukocyte interferons-alpha-B and -alpha-D. This is  
 CC hybrid B12D3D4 which correspond, in order, to the regions specified  
 CC starting with B1 (amino acids 1-60 of interferon-alpha-B). The hybrids  
 CC (P90185-90) act synergistically, in a compn. with muramyl peptide, to  
 CC treat virus infections in human and veterinary medicine, esp. herpes  
 CC simplex virus 1 and 2. They also reduce development of metastases from  
 CC some tumours eg B16-B16 melanoma or Lewis lung carcinoma.  
 SO Sequence 166 AA;  
 SQ 11 A; 13 R; 5 N; 11 D; 0 B; 6 C; 12 Q; 15 E; 0 Z; 2 G; 3 H;  
 SQ 8 I; 21 L; 9 K; 5 M; 9 F; 5 P; 11 S; 8 T; 2 W; 4 Y; 6 V;  
 Found using 'seq2' (09-424080.key)

106 vgetplmadslavkkyfrilrlyltekkykspcawevraeimsrlstnlqerlr  
 131 138  
 (7m--More--(2%) [m ... [K

1 match found in sequence:  
 P90398 ; Feline Interferon  
 (from "A-Geneseg 35.2")  
 ID P90398 standard; protein; 171 AA.  
 AC P90398;  
 DT 1-NOV-1989 (first entry)  
 DE Feline Interferon  
 KW Feline Interferon; peptide; antiviral agent; antitumour agent.  
 OS Feline  
 PN EP-322870-A.  
 PD 05-JUL-1987.  
 PF 27-DEC-1988; 121737.  
 PR 29-DEC-1987; JP-336297.  
 PA (TORA) Toray Industries Inc.  
 PI Yanai A, Nakamura N, Matsuda S;  
 DR WPI: 89-194216/27.  
 DT N-PSDB; N90185.  
 PT Feline Interferon gene, protein and precursor - used for obtaining  
 PT antiviral agents and antitumour agents for cats.  
 PS Claim 32; page 10 and fig 7; 18pp; English.  
 CC The sequence is the peptide derived from the feline interferon gene  
 CC (see N90185). The peptide may have an attached sugar chain.  
 CC Feline Interferon can be used as an antiviral and antitumour agent  
 CC for cats. It may be used to treat, eg FIVV, feline leukaemia,  
 CC feline viral rhinotracheitis, feline calicivirus disease and  
 CC feline infectious peritonitis. When not carrying a sugar chain,  
 CC the interferon has specific activity greater than 100000000 U/mg  
 CC and mol. wt. 20000 (suitable host cell is E.coli K12). With a

CC sugar chain, it has same activity and mol. wt. 24000 (suitable  
 CC host cells are COS 1, COS 7 and COS-DUK-XB-1).  
 CC See also N90186 and P90399.  
 SO Sequence 171 AA;  
 SQ 13 A; 13 R; 6 N; 8 D; 0 B; 6 C; 12 Q; 14 E; 0 Z; 6 G; 5 H;  
 SQ 5 I; 22 L; 7 K; 2 M; 8 F; 6 P; 14 S; 10 T; 2 W; 5 Y; 7 V;  
 Found using 'seq2' (09-424080.key)

110 apltnedlhpedsllrnyfgrlsllylqekkykspcawevraeimsrlstnlqerlr  
 135 142

1 match found in sequence:  
 P90399 ; Feline Interferon  
 (from "A-Geneseg 35.2")  
 ID P90399 standard; protein; 194 AA.  
 AC P90399;  
 DT 1-NOV-1989 (first entry)  
 DE Feline Interferon  
 KW Feline Interferon; peptide; antiviral agent; antitumour agent.  
 OS Feline  
 PN EP-322870-A.  
 PD 05-JUL-1989.  
 PF 27-DEC-1988; 121737.  
 PR 29-DEC-1987; JP-336297.  
 PA (TORA) Toray Industries Inc.  
 PI Yanai A, Nakamura N, Matsuda S;  
 DR WPI: 89-194216/27.  
 DT N-PSDB; N90186.  
 PT Feline Interferon gene, protein and precursor - used for obtaining  
 PT antiviral agents and antitumour agents for cats.  
 PS Claim 37; page 10 and fig 8; 18pp; English.  
 CC The sequence is the peptide sequence of feline interferon  
 CC precursor gene (see N90186). See also N90185 and P90398.  
 SO Sequence 194 AA;  
 SQ 16 A; 13 R; 7 N; 8 D; 0 B; 8 C; 12 Q; 14 E; 0 Z; 8 G; 5 H;  
 SQ 5 I; 27 L; 7 K; 3 M; 9 F; 7 P; 18 S; 10 T; 2 W; 5 Y; 10 V;  
 Found using 'seq2' (09-424080.key)

133 apltnedlhpedsllrnyfgrlsllylqekkykspcawevraeimsrlstnlqerlr  
 158 165

1 match found in sequence:  
 P80046 ; Sequence of human Interferon alpha-1 (huIFN alpha-1) encoded on  
 (from "A-Geneseg 35.2")  
 ID P80046 standard; protein; 167 AA.  
 AC P80046;  
 DT 17-NOV-1990 (first entry)  
 DE Sequence of human Interferon alpha-1 (huIFN alpha-1) encoded on  
 DE HindIII/EcoRI fragment of pgW5  
 KW Alpha-beta hybrid interferon; multi-class hybrid interferon;  
 KW antitumour; antiviral; therapy.  
 OS Homo sapiens.  
 PN USA4758428-A.  
 PD 19-JUL-1988.  
 PF 15-JUL-1985; 755265.  
 PR 15-JAN-1983; CA-419758.  
 PR 15-JUL-1985; US-755265,  
 PA (CETU) Cetus Corp.  
 PI Mark DF, Greasey AA;  
 DR WPI: 88-219882/31.  
 DT N-PSDB; n80043.

```

PF Multi-class hybrid interferon polypeptide(s)
PT having sequence from interferon-alpha-1 and sequence from
PS interferon-beta-1 for restricted activity
PS Example: Fig 3: 24pp; English.
CC Multi-class hybrid IFN polypeptides having an AA sequence composed
CC of 2 distinct subsequences are claimed. The plasmids used in the
CC construction of the huIFN alpha-1-beta-1 hybrid 1 are plasmids pGM5 and
CC pDM101/trp/beta-1 contg. the genes coding for huIFN alpha-1 and huIFN
CC beta-1 respectively. The plasmid pGM5 was constructed from the plasmid
CC pBR322 by substituting region between the EcoRI site to the PvuII site
CC with the E.coli trp promoter and the DNA sequence coding for the mature
CC protein of huIFN alpha-1.
SQ Sequence 167 AA:
SO 8 A; 12 R; 6 N; 11 D; 0 B; 5 C; 10 Q; 16 E; 0 Z; 3 G; 3 H;
SO 6 I; 22 L; 8 K; 8 M; 8 F; 13 S; 9 T; 2 W; 4 Y; 7 V;
Found using 'seq2' (09-424080.key)

```

```

17m--More--(3%) [m 107
|-----|
vgeplmvdslavkkyfrritlyltekkyapcawevraeimsrlstnlgelr
132 139

```

1 match found in sequence:

```

P80052 : Sequence of human interferon (huIFN) alpha-61A gene in p-alpha-61A
(from "A-Geneseg 35.2")
ID P80052 standard; protein: 167 AA.

```

```

AC P80052;
DT 17-NOV-1990 (first entry)
DE Sequence of human interferon (huIFN) alpha-61A gene in p-alpha-61A
KW Alpha-beta hybrid interferon; multi-class hybrid interferon;
KW antitumour; antiviral; therapy.
OS Homo sapiens.
PN US4758428-A.
PD 19-JUL-1988.
PF 15-JUL-1985; 755265.
PR 19-JAN-1983; CA-419758.
PR 15-JUL-1985; US-755265.
PA (CETR) Celus Corp.
PI Mark DF, Creasey AA;
DR MPI; 88-219882/31.
DR N-PSDB: n80049.
PT Multi-class hybrid interferon polypeptide(s)
PT having sequence from interferon-alpha-1 and sequence from
PT interferon-beta-1 for restricted activity
PS Example: Fig 16: 24pp; English.
CC Multi-class hybrid interferon polypeptides having an AA sequence composed
CC of 2 distinct subsequences are claimed. The plasmids used in the
CC construction of huIFN-alpha-61A-beta-1 hybrid are plasmids palpa61A and
CC pDM101/trp/beta-1. Assembly of the palpa61A plasmid involved replacing
CC the DNA fragment encoding the 23 AA signal polypeptide of preinterferon
CC with a 120bp EcoRI/Sau3A promoter fragment E.coli trp promoter, operator,
CC and trp leader ribosome binding site preoperator, encoding an ATG
CC initiation codon and using HindIII site that was inserted, 59 nucleotides
CC 3'-end of the TGA translational stop codon, to insert the gene into the
CC plasmid pBR11 (a deriv of pBR322 having a deletion between the HindIII
CC and PvuII sites). The complete DNA sequence of the promoter and gene
CC fragments inserted between the EcoRI and HindIII sites of pBR11 is shown
CC in n80049.
SQ Sequence 167 AA:
SO 8 A; 11 R; 6 N; 9 D; 0 B; 3 C; 13 Q; 13 E; 0 Z; 4 G; 4 H;
SO 7 I; 18 L; 8 K; 9 M; 10 F; 5 P; 14 S; 11 T; 2 W; 5 Y; 7 V;
Found using 'seq2' (09-424080.key)

```

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107 vedtplmvdslavkkyfrritlyltekkyapcawevraeimsrlstnlgelr
132 139

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...
-----
1 match found in sequence:
P80051 : Sequence of human interferon (huIFN)-beta-1 alpha-1 hybrid 1
(from "A-Geneseg 35.2")
ID P80051 standard; protein: 167 AA.

```

```

AC P80051;
DT 17-NOV-1990 (first entry)
DE 17m--More--(4%) [m [stic10%
stic10%
stic10% tail agen.res

```

```

Times: -- Search Statistics --
CPU Total Elapsed
00:00:40.09 00:01:18.00

```

```

Number of sequences searched: 170751
Number of sequence hits: 153
Number of separate matches: 153
Number of sequence hits saved: 0

```

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stic10%
script done on Tue Jan 15 10:33:02 2002

```





Script started on Tue Jan 15 10:39:04 2002

stic10% m pen.res

> 0 <  
0110 Intelligent

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "pen" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence "09-424080.key":

Selected sequence key from "09-424080.key":  
seq2 (AA) ID seq2 AA preliminary pattern

Followed by  
1 t o r r o r q o r m o r e o r g  
2 e o r r o r d o r l o r i o r a  
2 k o r r o r n o r m o r s o r e  
2 k o r r o r d o r n o r s  
2 y o r h  
2 s o r r o r d o r n o r a  
2 p o r r o r d o r l

Selected data banks and files:

Data bank : Pending\_AA , all entries

-- Output Parameters --

Format Options:	File Options:	Yes
Nucleic acid code matching	Exact	No
Find non-matching hits only	Indirect file	No
Report key used	Sequence or key file	No
Note position of hit	List of hits	No
Display full annotations	Hit display	Yes
Sequence context	Name and annotations	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

PCT-US00-01239-8 ; Sequence 8, Application PC/TUS0001239  
(from "/srch/paa/pctus\_COMB.pep")

Sequence 8, Application PC/TUS0001239

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Keratinocyte Derived Interferon

FILE REFERENCE: PP482P1

CURRENT APPLICATION NUMBER: PCT/US00/01239

EARLIER FILING DATE: 2000-01-20

EARLIER FILING DATE: 1998-07-21

EARLIER FILING DATE: 1999-07-21

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 8

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

154 161

1 match found in sequence:

PCT-US00-05881-828 ; Sequence 828, Application PC/TUS0005881  
(from "/srch/paa/pctus\_COMB.pep")

Sequence 828, Application PC/TUS0005881

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruden

TITLE OF INVENTION: Human Breast and Ovarian Cancer Associated Gene Sequences and P

FILE REFERENCE: PA103PCT

CURRENT APPLICATION NUMBER: PCT/US00/05881

CURRENT FILING DATE: 2000-03-08

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 846

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 828

LENGTH: 78

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (43)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (56)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Found using 'seq2' (09-424080.key)

1 LVFTETLREHKFMGFLMMLTLGIMSYSSLSLNNVKKHCSQRXLLSTAINHG

21 28

1 match found in sequence:

PCT-US00-05988-1444 ; Sequence 1444, Application PC/TUS0005988  
(from "/srch/paa/pctus\_COMB.pep")

Sequence 1444, Application PC/TUS0005988

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruden

TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptide

FILE REFERENCE: PA101PCT

CURRENT APPLICATION NUMBER: PCT/US00/05988

EARLIER FILING DATE: 2000-03-08

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 1444

LENGTH: 531

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (6)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (446)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (474)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE  
 LOCATION: (502)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (504)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 Found using 'seq2' (09-424080.key)

16 SPSPEIYNSEGRKLTREFFTRKRLCEERHNLITEMVALNPDEKPPADKKPATRYS  
 41 48

match found in sequence:  
 PCT-US00-07285-106 ; Sequence 106, Application PC/TUS0007285  
 (from "/srch/paa/pcTUS\_COMB.pep")  
 Sequence 106, Application PC/TUS0007285  
 GENERAL INFORMATION:  
 APPLICANT: Valenzuela, Dario  
 APPLICANT: Yuan, Olive  
 APPLICANT: Hoffman, Heidi  
 APPLICANT: Hall, Jeff  
 APPLICANT: Rappieko, Peter  
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 \* FILE REFERENCE: GI 6919X  
 CURRENT APPLICATION NUMBER: PCT/US00/07285  
 CURRENT FILING DATE: 2000-03-17  
 NUMBER OF SEQ ID NOS: 194  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 106  
 LENGTH: 431  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)

17m-More--(0%) [m ... [K  
 ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)

387 IGSLEFGLVLYGLVLLGRILSESLRRKRRSRDLYLINGIYVDI  
 412 419

match found in sequence:  
 PCT-US00-08982-108 ; Sequence 108, Application PC/TUS0008982  
 (from "/srch/paa/pcTUS\_COMB.pep")  
 Sequence 108, Application PC/TUS0008982  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 TITLE OF INVENTION: 48 Human Secreted Proteins  
 FILE REFERENCE: PS542PCT  
 CURRENT APPLICATION NUMBER: PCT/US00/08982  
 CURRENT FILING DATE: 2000-04-06  
 EARLIER APPLICATION NUMBER: 60/128,696  
 EARLIER FILING DATE: 1999-04-09  
 EARLIER APPLICATION NUMBER: 60/176,069  
 EARLIER FILING DATE: 2000-01-14  
 NUMBER OF SEQ ID NOS: 142  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 108  
 LENGTH: 66  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)

1 LSPRLGSGAISAHCKRLRLTDSRHSPASACSWDYKRRPPRRGQLSVSVEM  
 19 26

1 match found in sequence:  
 PCT-US00-08983-141 ; Sequence 141, Application PC/TUS0008983  
 (from "/srch/paa/pcTUS\_COMB.pep")  
 Sequence 141, Application PC/TUS0008983  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 TITLE OF INVENTION: 50 Human Secreted Proteins  
 FILE REFERENCE: PS543PCT  
 CURRENT APPLICATION NUMBER: PCT/US00/08983  
 CURRENT FILING DATE: 2000-04-06  
 EARLIER APPLICATION NUMBER: 60/128,703  
 EARLIER FILING DATE: 1999-04-09  
 EARLIER APPLICATION NUMBER: 60/176,068  
 EARLIER FILING DATE: 2000-01-20  
 NUMBER OF SEQ ID NOS: 152  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 141  
 LENGTH: 372  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)

75 SSSSLASGEFTGVKELDISQETIAQLQRRKSLLEODIREKEBAIKQTSFVQELQNDL  
 17m-More--(0%) [m 100 107

1 match found in sequence:  
 PCT-US00-08983-142 ; Sequence 142, Application PC/TUS0008983  
 (from "/srch/paa/pcTUS\_COMB.pep")  
 Sequence 142, Application PC/TUS0008983  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 TITLE OF INVENTION: 50 Human Secreted Proteins  
 FILE REFERENCE: PS543PCT  
 CURRENT APPLICATION NUMBER: PCT/US00/08983  
 CURRENT FILING DATE: 2000-04-06  
 EARLIER APPLICATION NUMBER: 60/128,703  
 EARLIER FILING DATE: 1999-04-09  
 EARLIER APPLICATION NUMBER: 60/176,068  
 EARLIER FILING DATE: 2000-01-20  
 NUMBER OF SEQ ID NOS: 152  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 142  
 LENGTH: 371  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)

75 SSGSLASGEFTGVKELDISQETIAQLQRRKSLLEODIREKEBAIKQTSFVQELQNDL  
 100 107

1 match found in sequence:  
 PCT-US00-26524B-6953 ; Sequence 6953, Application PC/TUS0026524B  
 (from "/srch/paa/pcTUS\_COMB.pep")  
 Sequence 6953, Application PC/TUS0026524B

## GENERAL INFORMATION:

APPLICANT: Birse et. al.  
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

FILE REFERENCE: PA005PCT  
CURRENT APPLICATION NUMBER: PCT/US00/26524B

CURRENT FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6953

LENGTH: 92

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

(7m--More--(0%)) [m [K

...

1 match found in sequence:

PCT-US01-35017A-1414 ; Sequence 1414, Application PC/TUS0035017A  
(from "/src/paa/PCTUS\_COMB.pep")

Sequence 1414, Application PC/TUS0035017A

GENERAL INFORMATION:

APPLICANT: Hyseq Inc

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 784PCT

CURRENT APPLICATION NUMBER: PCT/US00/35017A

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US09/552,317

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478

SEQ ID NO 1414

LENGTH: 365

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

...

1 match found in sequence:

PCT-US01-00663-28110 ; Sequence 28110, Application PC/TUS0100663  
(from "/src/paa/PCTUS\_COMB.pep")

Sequence 28110, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 03 August 2000 (03.08.00)  
PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 28110

LENGTH: 47

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

...

1 match found in sequence:

PCT-US01-00663-31537 ; Sequence 31537, Application PC/TUS0100663  
(from "/src/paa/PCTUS\_COMB.pep")

Sequence 31537, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 31537

LENGTH: 751

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

572 SSSLQOEELEELKSLQEKDATTITLOENNRHLSDSIAATSELERHEQTDSEIKOL  
597 564

1 match found in sequence:

PCT-US01-00663-34035 ; Sequence 34035, Application PC/TUS0100663  
(from "/src/paa/PC/TUS-COMB.pep")

Sequence 34035, Application PC/TUS0100663  
GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 34035

LENGTH: 75

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC004614.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2

OTHER INFORMATION: SWISSPROT HIT: P45702, EVALU 1.80e+00

OTHER INFORMATION: EST HUMAN HIT: AA249238.1, EVALU 6.60e-01

Found using 'seq2' (09-424080.key)

Found using 'seq2' (09-424080.key)

[7m--More--(0%) [m 11 TEIWSMSKKEGRIKNGLEKMLALRLRRHAPGIGWRPKNMGTKRAKALRIAAYIV  
36 43

1 match found in sequence:

PCT-US01-00663-34955 ; Sequence 34955, Application PC/TUS0100663  
(from "/src/paa/PC/TUS-COMB.pep")

Sequence 34955, Application PC/TUS0100663  
GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 34955

LENGTH: 69

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AL133229.19

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4

OTHER INFORMATION: SWISSPROT HIT: P16543, EVALU 3.40e+00

Found using 'seq2' (09-424080.key)

Found using 'seq2' (09-424080.key)

1 MGATAVAVALGYIRGVGPALIOSLEASHRLILNLSSTENRGNRSLAVLRMTLVRT  
25 32

1 match found in sequence:

PCT-US01-00663-38470 ; Sequence 38470, Application PC/TUS0100663  
(from "/src/paa/PC/TUS-COMB.pep")

Sequence 38470, Application PC/TUS0100663  
GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

[7m--More--(0%) [m [kstic10%

stic10%

stic10% tail pen.res

-- Search Statistics --

Times: CPU 00:23:34.02 Total Elapsed 00:31:00.00

Number of sequences searched: 3293760

Number of sequence hits: 1411

Number of separate matches: 1413

Number of sequence hits saved: 0

stic10%

script done on Tue Jan 15 10:39:19 2002

Script started on Tue Jan 15 10:33:19 2002  
 sctid0% m iss.res

> 0 <  
 01/00 Intelligenetics  
 > 0 <

Quest - Quick User-directed Expression Search Tool  
 Release 5.4

-- Outline of search "Iss" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "09-424080.key":

Selected sequence key from "09-424080.key":

seq2 (AA) ID seq2 AA preliminary pattern

followed by

```

1 1
2 1
2 t o r o r q o r m o r e o r g
2 e o r r o r d o r l o r l o r a
2 k o r r o r n o r m o r s o r e
2 k o r r o r d o r n o r s
2 y o r h
2 s o r r o r d o r n o r a
2 p o r r o r d o r l

```

Selected data banks and files:

Data bank : Issued\_AA , all entries

-- Output Parameters --

Format Options:	File Options:
Nucleic acid code matching	Exact
Find non-matching hits only	No
Report key used	Yes
Note position of hit	Yes
Display full annotations	Yes
Sequence context	25

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

US-08-062-368-2 ; Sequence 2, Application US/08062368

from "srch/laa/5A.COMB.pep")

Sequence 2, Application US/08062368

Patent No. 5491086

GENERAL INFORMATION:

APPLICANT: Gelfand, David H.

APPLICANT: Wang, Alice M.

TITLE OF INVENTION: Purified Thermostable Nucleic Acid

TITLE OF INVENTION: Polymerases Enzyme From Pyrodicticum Species

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/062,368

FILING DATE: 19930514

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sias Ph.D., Stacey R.

REGISTRATION NUMBER: 32,630

REFERENCE/DOCKET NUMBER: 8584

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 814-2863

TELEFAX: (510) 814-2977

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 803 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

Found using 'seq2' (09-424080.key)

194 RGSPNPSRDPVILISIKDSKGNKLEANNYDKNVLRFFIETIRSRDPDIYGYNSN  
 219 226

1 match found in sequence:

US-08-286-888B-1 ; Sequence 1, Application US/08286888B

(from "srch/laa/5A.COMB.pep")

Sequence 1, Application US/08286888B

Patent No. 5627024

GENERAL INFORMATION:

APPLICANT: Maruyama, Ichiro

APPLICANT: Maruyama, Hiroko

APPLICANT: Brenner, Sydney

TITLE OF INVENTION: LAMBDOID BACTERIOPHAGE VECTORS FOR

TITLE OF INVENTION: EXPRESSION OF FOREIGN PROTEINS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5627024th Torrey Pines Road, TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,888B

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 432.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-6312

TELEFAX: 619-554-2937

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

Found using 'seq2' (09-424080.key)

25 DPYANPLSDVMSRLAKVKDLTPGELTAESYDSDYLDDEDADMTATGOGOKSAGDTSF  
50 57

1 match found in sequence:  
US-08-286-888B-6; Sequence 6, Application US/08286888B  
(from "/srch/laa/5A.COMB.pep")  
Sequence 6, Application US/08286888B  
Patent No. 5627024

GENERAL INFORMATION:  
APPLICANT: Maruyama, Ichiro  
APPLICANT: Maruyama, Hiroko  
APPLICANT: Brenner, Sydney  
TITLE OF INVENTION: LAMBDOID BACTERIOPHAGE VECTORS FOR  
TITLE OF INVENTION: EXPRESSION OF FOREIGN PROTEINS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5627024th Torrey Pines Road, TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,888B  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 432.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312

[7m--More--(3%) (m TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 292 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: peptide  
LOCATION: 177  
OTHER INFORMATION: /label= Xaa  
OTHER INFORMATION: /note= "Wherein Xaa is a suppressor termination  
Found using seq2' (09-424080.key)

25 DPYANPLSDVMSRLAKVKDLTPGELTAESYDSDYLDDEDADMTATGOGOKSAGDTSF  
50 57

1 match found in sequence:  
US-08-294-386C-1; Sequence 1, Application US/08294386C  
(from "/srch/laa/5A.COMB.pep")  
Sequence 1, Application US/08294386C  
Patent No. 5646030  
GENERAL INFORMATION:  
APPLICANT: Ray, Bryan L.

APPLICANT: Lin, Edmund C.C.  
APPLICANT: Crea, Roberto  
TITLE OF INVENTION: Method Of Isolating Mutant Cells  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/294,386C  
FILING DATE: August 23, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: SYZ-010CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/330-1300  
TELEFAX: 617/330-1311

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 246 amino acids  
TYPE: amino acid  
TOPOLOGY: linear STRANDEDNESS: single  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
Found using 'seq2' (09-424080.key)

25 DPYANPLSDVMSRLAKVKDLTPGELTAESYDSDYLDDEDADMTATGOGOKSAGDTSF  
50 57

1 match found in sequence:  
US-08-294-386C-3; Sequence 3, Application US/08294386C  
(from "/srch/laa/5A.COMB.pep")  
Sequence 3, Application US/08294386C  
Patent No. 5646030  
GENERAL INFORMATION:  
APPLICANT: Ray, Bryan L.  
APPLICANT: Lin, Edmund C.C.  
APPLICANT: Crea, Roberto  
TITLE OF INVENTION: Method Of Isolating Mutant Cells  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/294,386C  
FILING DATE: August 23, 1994

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kerner, Ann-Louise  
 REGISTRATION NUMBER: 33,523  
 REFERENCE/DOCKET NUMBER: SYZ-010CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/330-1300  
 TELEFAX: 617/330-1311  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 246 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 Found using 'seq2' (09-424080.key)

7m--More--(5%) [m [K  
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 DRYANPLSDVDWSRLAKVKDLTPGELTAESYDDSYLDDEDADMTATGGGQKSAGDTSF  
 50 57

1 match found in sequence:  
 US-08-299-249A-1; Sequence 1, Application US/08299249A

(From "/srch/laa/5A\_COMB.pep")  
 Sequence 1, Application US/08299249A  
 Patent No. 5650267

# GENERAL INFORMATION:

\* APPLICANT: RAY, Bryan L.; and  
 TITLE OF INVENTION: Method Of Detecting Compounds  
 TITLE OF INVENTION: Utilizing Genetically Modified  
 TITLE OF INVENTION: Lambdaoid Bacteriophage  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: HALE and DORR  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: U.S.A.  
 ZIP: 02109

# COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/299,249A

FILING DATE: 31-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,865

FILING DATE: 27-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: SYZ-011FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/526-6000

TELEFAX: 617/526-5000

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide  
 HYPOTHEICAL: YES  
 Found using 'seq2' (09-424080.key)

25 DRYANPLSDVDWSRLAKVKDLTPGELTAESYDDSYLDDEDADMTATGGGQKSAGDTSF  
 |-----|  
 7m--More--(6%) [m [Kstic10% 50 57

stic10%  
 stic10%  
 stic10% tail iss.res

-- Search Statistics --

Times: CPU 00:01:58.07 Total Elapsed 00:04:44.00

Number of sequences searched: 212306

Number of sequence hits: 124

Number of separate matches: 124

Number of sequence hits saved: 0

stic10%  
 script done on Tue Jan 15 10:33:31 2002

1

2

1

2



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:35:33 ; Search time 19.95 Seconds  
(without alignments)  
9.024 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42  
Sequence: 1 LTRKXSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Maximum number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database : Issued Patents-AA:\*

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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	2	US-08-669-284B-30
2	42	100.0	11	1	US-08-362-453-4
3	42	100.0	18	1	US-08-362-453-5
4	42	100.0	150	1	US-08-362-453-10
5	42	100.0	150	1	US-08-362-453-11
6	42	100.0	150	1	US-08-362-453-12
7	42	100.0	162	1	US-08-362-453-15
8	42	100.0	165	1	US-08-362-453-13
9	42	100.0	165	1	US-08-362-453-14
10	42	100.0	166	1	US-08-362-453-8
11	42	100.0	166	1	US-08-362-453-9
12	42	100.0	166	2	US-08-489-066A-16
13	42	100.0	166	3	US-08-489-072A-16
14	42	100.0	166	3	US-08-819-238A-2
15	42	100.0	166	4	US-08-954-395A-9
16	42	100.0	166	4	US-08-954-395A-10
17	42	100.0	166	4	US-08-954-395A-11
18	42	100.0	166	4	US-08-954-395A-12
19	42	100.0	166	4	US-08-954-395A-13
20	42	100.0	166	4	US-08-954-395A-14
21	42	100.0	166	4	US-08-954-395A-15
22	42	100.0	166	4	US-08-954-395A-16
23	42	100.0	166	4	US-08-954-395A-17
24	42	100.0	166	4	US-08-489-071A-16
25	42	100.0	166	4	US-09-339-913B-75
26	42	100.0	166	4	US-09-339-913B-76
27	42	100.0	166	4	US-09-339-913B-77

28	42	100.0	166	4	US-09-339-913B-79	Sequence 79, Appl
29	42	100.0	166	4	US-09-339-913B-80	Sequence 80, Appl
30	42	100.0	166	4	US-09-339-913B-83	Sequence 83, Appl
31	42	100.0	166	4	US-09-339-913B-84	Sequence 84, Appl
32	42	100.0	166	4	US-09-339-913B-85	Sequence 85, Appl
33	42	100.0	189	1	US-08-026-758-1	Sequence 1, Appl
34	42	100.0	189	1	US-08-026-758-2	Sequence 2, Appl
35	42	100.0	189	1	US-08-026-758-3	Sequence 3, Appl
36	42	100.0	189	1	US-08-026-758-6	Sequence 6, Appl
37	42	100.0	189	1	US-08-026-758-7	Sequence 7, Appl
38	42	100.0	189	1	US-08-026-758-11	Sequence 11, Appl
39	42	100.0	189	1	US-08-026-758-16	Sequence 16, Appl
40	42	100.0	189	1	US-08-026-758-17	Sequence 17, Appl
41	42	100.0	189	1	US-08-026-758-19	Sequence 19, Appl
42	42	100.0	189	1	US-08-026-758-20	Sequence 20, Appl
43	42	100.0	189	2	US-08-489-066A-2	Sequence 2, Appl
44	42	100.0	189	3	US-08-489-072A-2	Sequence 11, Appl
45	42	100.0	189	4	US-09-206-935-8	Sequence 8, Appl
46	42	100.0	189	4	US-09-206-935-10	Sequence 10, Appl
47	42	100.0	189	4	US-09-206-935-11	Sequence 11, Appl
48	42	100.0	189	4	US-09-206-935-12	Sequence 12, Appl
49	42	100.0	189	4	US-09-206-935-18	Sequence 18, Appl
50	42	100.0	189	4	US-09-206-935-19	Sequence 19, Appl

#### ALIGNMENTS

RESULT 1  
US-08-669-284B-30  
; Sequence 30, Application US/08669284B  
; Patent No. 5939534  
; GENERAL INFORMATION:  
; APPLICANT: Inoue, Makoto  
; APPLICANT: Kikuchi, Kaoru  
; APPLICANT: Ishige, Yoko  
; APPLICANT: Ito, Akira  
; APPLICANT: Kimura, Toru  
; APPLICANT: Nakayama, Chikao  
; APPLICANT: No. 5939534uchl, Hiroshi  
; TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,284B  
; FILING DATE: 28-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/02269  
; FILING DATE: 27-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 06-268281  
; FILING DATE: 05-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 06-201504  
; FILING DATE: 02-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 05-350934  
; FILING DATE: 29-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakamura, Dean H.  
; REGISTRATION NUMBER: 33,981  
; REFERENCE/DOCKET NUMBER: Q-42041

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-284B-30

Query Match 100.0%; Score 42; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
b 1 LTERKYS 8

RESULT 2  
US-08-362-453-4  
Sequence 4, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-362-453-4

Query Match 100.0%; Score 42; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0064;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
Db 2 LTERKYS 9

RESULT 3  
US-08-362-453-5  
Sequence 5, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-362-453-5

Query Match 100.0%; Score 42; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
Db 9 LTERKYS 16

RESULT 4  
US-08-362-453-10  
Sequence 10, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington



Query Match 100.0%; Score 42; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
Db 126 LTERKXSP 133

## RESULT 7

US-08-362-453-15  
; Sequence 15, Application US/08362453  
; Patent No. 5684129  
; GENERAL INFORMATION:  
; APPLICANT: FISH, Eleanor N.  
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,453  
; FILING DATE: 06-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/909,739  
; APPLICATION NUMBER: FILING DATE: 07-JUL-1992  
; APPLICATION NUMBER: US 07/980,525  
; APPLICATION NUMBER: FILING DATE: 20-NOV-1992  
; APPLICATION NUMBER: PCT/CA93/00279  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kites, Monica Chin  
; REGISTRATION NUMBER: 36,105  
; REFERENCE/DOCKET NUMBER: P638-4017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-5000  
; TELEFAX: (202) 638-4810  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 162 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-362-453-15

Query Match 100.0%; Score 42; DB 1; Length 162;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
Db 127 LTERKXSP 134

## RESULT 8

US-08-362-453-13  
; Sequence 13, Application US/08362453  
; Patent No. 5684129  
; GENERAL INFORMATION:  
; APPLICANT: FISH, Eleanor N.  
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES

NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,453  
; FILING DATE: 06-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/909,739  
; APPLICATION NUMBER: FILING DATE: 07-JUL-1992  
; APPLICATION NUMBER: US 07/980,525  
; APPLICATION NUMBER: FILING DATE: 20-NOV-1992  
; APPLICATION NUMBER: PCT/CA93/00279  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kites, Monica Chin  
; REGISTRATION NUMBER: 36,105  
; REFERENCE/DOCKET NUMBER: P638-4017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-5000  
; TELEFAX: (202) 638-4810  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 165 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-362-453-13

Query Match 100.0%; Score 42; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
Db 130 LTERKXSP 137

## RESULT 9

US-08-362-453-14  
; Sequence 14, Application US/08362453  
; Patent No. 5684129  
; GENERAL INFORMATION:  
; APPLICANT: FISH, Eleanor N.  
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,453  
; FILING DATE: 06-JAN-1995  
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
08-362-453-14

Query Match 100.0%; Score 42; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 130 LTERKXSP 137

RESULT 10  
US-08-362-453-8  
Sequence 8, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids

TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-8

Query Match 100.0%; Score 42; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 131 LTERKXSP 138

RESULT 11  
US-08-362-453-9  
Sequence 9, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-9

Query Match 100.0%; Score 42; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 131 LTERKXSP 138

RESULT 12  
US-08-489-066A-16

; Sequence 16, Application US/08489066A  
; Patent No. 5869293  
; GENERAL INFORMATION:  
; APPLICANT: PESTKA, SIDNEY  
; TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,  
; INTERLEUKINS, ET AL.  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/489,066A  
; FILING DATE: 09-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/257,784  
; FILING DATE: 10-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,231  
; FILING DATE: 11-JUN-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fehner, Ph.D., Esq., Paul F.  
; REGISTRATION NUMBER: 35,135  
; REFERENCE/DOCKET NUMBER: 1705-1-002 CIPC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; IMMEDIATE SOURCE:  
; CLONE: Hu-IFN-alpha001  
; US-08-489-066A-16

Query Match 100.0%; Score 42; DB 2; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKKYSP 8  
|11111111|  
DB 131 LTERKKYSP 138

RESULT 13  
US-08-489-072A-16  
; Sequence 16, Application US/08489072A  
; Patent No. 6001589  
; GENERAL INFORMATION:  
; APPLICANT: PESTKA, SIDNEY  
; TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,  
; INTERLEUKINS, ET AL.  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack

; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/489,072A  
; FILING DATE: 09-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/257,784  
; FILING DATE: 10-JUN-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,231  
; FILING DATE: 11-JUN-1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fehner, Ph.D., Esq., Paul F.  
; REGISTRATION NUMBER: 35,135  
; REFERENCE/DOCKET NUMBER: 1705-1-002 CIPA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; IMMEDIATE SOURCE:  
; CLONE: Hu-IFN-alpha001  
; US-08-489-072A-16

Query Match 100.0%; Score 42; DB 3; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKKYSP 8  
|11111111|  
DB 131 LTERKKYSP 138

RESULT 14  
US-08-819-238A-2  
; Sequence 2, Application US/08819238A  
; Patent No. 6069133  
; GENERAL INFORMATION:  
; APPLICANT: Henry C. Chlou and Dennis J. Carlo  
; TITLE OF INVENTION: TARGETED DELIVERY OF GENES ENCODING  
; INTERFERON  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: LAHYE & COCKFIELD, LLP  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/819,238A  
; FILING DATE:

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/616,023  
FILING DATE: 14 MARCH 1996  
APPLICATION NUMBER: PCT/US96/  
FILING DATE: 14 MARCH 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: REMILLARD, JANE E.  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: TTI-143CPC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-08-819-238A-2

Query Match 100.0%; Score 42; DB 3; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 15  
US-08-954-395A-9  
Sequence 9, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
LIBRARY: Genbank Accessn. J00210, PID 9386796  
CLONE: Human IFN alpha-d, mature protein  
US-08-954-395A-9

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 16  
US-08-954-395A-10  
Sequence 10, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N0  
US-08-954-395A-10

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 17  
US-08-954-395A-11  
Sequence 11, Application US/08954395A  
Patent No. 6204022

## GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelie H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
TITLE OF INVENTION: ANALOG  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N1  
US-08-954-395A-11

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 18  
US-08-954-395A-12  
Sequence 12, Application US/08954395A  
Patent No. 6204022

## GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelie H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
TITLE OF INVENTION: ANALOG  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N2  
US-08-954-395A-12

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 19  
US-08-954-395A-13  
Sequence 13, Application US/08954395A



Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N3  
US-08-954-395A-13

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYSK 8  
Db 131 LTERKYSK 138

RESULT 20  
US-08-954-395A-14  
Sequence 14, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.

APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N4  
US-08-954-395A-14

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYSK 8  
Db 131 LTERKYSK 138

RESULT 21  
US-08-954-395A-15  
Sequence 15, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N5  
US-08-954-395A-15

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
DB 131 LTRKXSP 138

RESULT 22

US-08-954-395A-16  
Sequence 16, Application US/08954395A  
Patent No. 6204022

GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelie H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A

FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N6  
US-08-954-395A-16

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
DB 131 LTRKXSP 138

RESULT 23

US-08-954-395A-17  
Sequence 17, Application US/08954395A  
Patent No. 6204022

GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelie H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N7  
US-08-954-395A-17

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
|||||||  
131 LTERKYS 138

RESULT 24  
US-08-489-071A-16  
Sequence 16, Application US/08489071A  
Patent No. 6300474  
GENERAL INFORMATION:  
APPLICANT: PESTKA, SIDNEY  
TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,  
TITLE OF INVENTION: INTERLEUKINS, ET AL.  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klaiber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/489,071A  
FILING DATE: 09-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/257,784  
FILING DATE: 10-JUN-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/076,231  
FILING DATE: 11-JUN-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehner, Ph.D., Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: 1705-1-002 CIPC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

IMMEDIATE SOURCE:  
CLONE: Hu-IFN-alpha001  
US-08-489-071A-16

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
|||||||  
Db 131 LTERKYS 138

RESULT 25  
US-09-339-913B-75  
Sequence 75, Application US/09339913B  
Patent No. 6303344  
GENERAL INFORMATION:  
APPLICANT: Patlen, Phillip  
APPLICANT: Stemmer, William P.C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING  
FILE REFERENCE: 02-020503US  
CURRENT APPLICATION NUMBER: US/09/339,913B  
CURRENT FILING DATE: 1999-06-24  
PRIOR APPLICATION NUMBER: 08/769,062  
PRIOR FILING DATE: 1996-12-18  
PRIOR APPLICATION NUMBER: 08/198,431  
PRIOR FILING DATE: 1994-02-17  
PRIOR APPLICATION NUMBER: 08/425,684  
PRIOR FILING DATE: 1995-04-18  
PRIOR APPLICATION NUMBER: 08/537,874  
PRIOR FILING DATE: 1995-10-30  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 75  
LENGTH: 166  
TYPE: PRT  
ORGANISM: consensus alpha interferon  
US-09-339-913B-75

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
|||||||  
Db 131 LTERKYS 138

Search completed: January 15, 2002, 08:40:28  
Job time: 295 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:40:34 ; Search time 35.65 Seconds  
(without alignments)  
32.824 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTRKXSP 8

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database :

1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP:phage:\*  
10: SP:plant:\*  
11: SP:rodent:\*  
12: SP:virus:\*  
13: SP:vertebrate:\*  
14: SP\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	166	4 Q9UMJ3	Q9UMJ3 homo sapien
2	42	100.0	181	4 Q14608	Q14608 homo sapien
3	42	100.0	189	4 Q14605	Q14605 homo sapien
4	42	100.0	189	4 Q14639	Q14639 homo sapien
5	42	100.0	189	4 Q14607	Q14607 homo sapien
6	36	85.7	108	6 Q9N106	Q9N106 equus caball
7	36	85.7	170	6 Q29114	Q29114 sus scrofa
8	36	85.7	170	6 Q29115	Q29115 sus scrofa
9	36	85.7	730	10 Q9S9M5	Q9S9M5 arabidopsis
10	34	81.0	181	3 Q13619	Q13619 schizosach
11	34	81.0	577	5 Q35995	Q35995 vaitimorpha
12	34	81.0	1154	5 Q9V6S9	Q9V6S9 drosophila
13	33	78.6	110	10 Q9SXY5	Q9SXY5 arabidopsis
14	33	78.6	334	2 Q9CKT2	Q9CKT2 pasteurella
15	33	78.6	767	11 Q9WTU7	Q9WTU7 mus musculu
16	32	76.2	83	5 Q9V8W6	Q9V8W6 drosophila
17	32	76.2	400	5 Q9VBY9	Q9VBY9 drosophila
18	32	76.2	414	10 Q9SX74	Q9SX74 arabidopsis
19	32	76.2	573	5 Q23323	Q23323 caenorhabdi

20	32	76.2	1528	5 Q95022	Q95022 cryptospori
21	31	73.8	60	12 Q9IEU9	Q9IEU9 cotton leaf
22	31	73.8	113	2 Q9F554	Q9F554 escherichia
23	31	73.8	118	12 Q88551	Q88551 tomato yell
24	31	73.8	118	12 Q73583	Q73583 cotton leaf
25	31	73.8	118	12 Q9QDF8	Q9QDF8 tomato leaf
26	31	73.8	118	12 Q9IGY3	Q9IGY3 tobacco lea
27	31	73.8	118	12 Q9IGX7	Q9IGX7 tobacco gem
28	31	73.8	118	12 Q99DR5	Q99DR5 chili leaf
29	31	73.8	136	11 Q61717	Q61717 mus musculu
30	31	73.8	176	11 Q9D380	Q9D380 mus musculu
31	31	73.8	190	11 Q61716	Q61716 mus musculu
32	31	73.8	190	11 Q61718	Q61718 mus musculu
33	31	73.8	190	11 Q61719	Q61719 mus musculu
34	31	73.8	197	2 Q06983	Q06983 bacillus su
35	31	73.8	199	4 Q9Y6M8	Q9Y6M8 homo sapien
36	31	73.8	201	2 Q45137	Q45137 bacteroides
37	31	73.8	239	2 Q9ZAD2	Q9ZAD2 escherichia
38	31	73.8	261	2 P96679	P96679 bacillus su
39	31	73.8	275	2 P94124	P94124 acinetobact
40	31	73.8	285	3 Q00875	Q00875 fusarium so
41	31	73.8	322	4 Q92780	Q92780 homo sapien
42	31	73.8	401	1 Q59114	Q59114 pyrococcus
43	31	73.8	439	2 Q9RCV4	Q9RCV4 salmonella
44	31	73.8	510	2 Q9RK66	Q9RK66 streptomyce
45	31	73.8	589	2 Q9RMV4	Q9RMV4 bacillus an
46	31	73.8	603	2 Q9L217	Q9L217 streptomyce
47	31	73.8	727	3 Q9P6M8	Q9P6M8 schizosach
48	31	73.8	804	3 Q00089	Q00089 aspergillus
49	31	73.8	804	3 Q93933	Q93933 aspergillus
50	31	73.8	893	2 Q9X1G2	Q9X1G2 thermotoga

## ALIGNMENTS

RESULT	ID	Q9UMJ3	PRELIMINARY;	PRT;	166 AA.
AC	Q9UMJ3	Q9UMJ3	Q9UMJ3	Q9UMJ3	Q9UMJ3
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE	IFNA	PROTEIN (FRAGMENT).			
GN	IFNA				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.				
RA	Medline-8329241; Pubmed-6310510;				
RT	Weber H., Weissmann C.;				
RT	"Formation of genes coding for hybrid proteins by recombination				
RT	between related, cloned genes in E. coli."				
RL	Nucleic Acids Res. 11:5661-5669(1983).				
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA				
CC	FAMILY.				
DR	EMBL; M29884; AAA52714.1; -.				
DR	HSSP; P01563; ZHIE.				
DR	Interpro; IPR000471; Interferon_abd.				
DR	Pfam; PF00143; Interferon_1.				
DR	PRINTS; PR00266; INTERFERONAB.				
DR	Prodom; PD000550; Interferon_abd. 1.				
DR	SMART; SM00076; IFabd. 1.				
DR	PROSITE; PS00252; INTERFERON_A-B-D; 1.				
DR	Antiviral; Cytochrome.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE	166 AA;	19386 MW;	4152EA2A78361BB8	CRC64;

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.65;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
DB 131 LTRKXSP 138

## RESULT 2

Q14608 PRELIMINARY; PRT; 181 AA.  
AC Q14608;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE LEUCOCYTE INTERFERON-ALPHA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NX NCB1\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85056523; PubMed=6548765;  
RA Gren E., Berzin V.M., Jansone I., Tsimanis A., Vishnevsky Y.,  
RA Apsalons U.;  
RT "Novel human leukocyte interferon subtype and structural comparison of  
RT alpha interferon genes.";  
RL J. Interferon Res. 4:609-617(1984).  
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.  
CC EMBL; M28586; AAA36041.1; -.  
DR HSSP; P01563; 2ITE.  
DR Interpro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon\_1.  
DR PRINTS: PR00266; INTERFERONAB.  
DR Prodom: PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Antiviral; Cytokine; Signal.  
SQ SEQUENCE 181 AA; 20878 MW; 3DB45120764EBABC CRC64;

Query Match 100.0%; Score 42; DB 4; Length 181;  
Best Local Similarity 100.0%; Pred. No. 0.71;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
DB 146 LTRKXSP 153

## RESULT 3

Q14605 PRELIMINARY; PRT; 189 AA.  
AC Q14605;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE INTERFERON-ALPHA 13 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCB1\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RA Rostoks N.;  
RL Submitted (JAN-1994) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86037205; PubMed=4057246;  
RA Hencho K., Brosius J., Fujisawa A., Fujisawa J.T., Haynes J.R.,  
RA Hochstadt J., Kovacic T., Pasek M., Schambeck A., Schmid J.,  
RA Toookuro K., Waelchli M., Nagata S., Weissmann C.;  
RT "Structural relationship of human interferon alpha genes and

RT pseudogenes.";  
RL J. Mol. Biol. 185:227-260(1985).

CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA

CC FAMILY.  
CC EMBL; X75934; CAA53538.1; -.  
DR EMBL; A07163; CAA00632.1; -.  
DR HSSP; P01563; 2ITE.  
DR Interpro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon\_1.  
DR PRINTS: PR00266; INTERFERONAB.  
DR Prodom: PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Antiviral; Cytokine; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 189  
FT POTENTIAL.  
SQ SEQUENCE 189 AA; 21697 MW; 442F8B8754D88398 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.74;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
DB 154 LTRKXSP 161

## RESULT 4

Q14639 PRELIMINARY; PRT; 189 AA.  
AC Q14639;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE LEUCOCYTE INTERFERON PRECURSOR.  
GN IFNA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCB1\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87024453; PubMed=3767336;  
RA Saveliev V.I., Zlochevsky M.L., Sorokin A.V., Naroditskaya V.A.,  
RA Bolotin A.P., Demyanova N.G., Kozlov Y.I., Nezanov N.S.,  
RA Gazaryan K.G., Monastyrskaya G.S., Sverdlov E.D.;  
RT "[Cloning and the determination of the nucleotide sequences in 2 genes  
RT of human leukocyte interferons].";  
RL Antibiot. Med. Biotechnol. 31:592-596(1986).  
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.  
CC EMBL; M38289; AAA59165.1; -.  
DR HSSP; P01563; 2ITE.  
DR Interpro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon\_1.  
DR PRINTS: PR00266; INTERFERONAB.  
DR Prodom: PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Antiviral; Cytokine; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 189  
FT POTENTIAL.  
SQ SEQUENCE 189 AA; 21781 MW; 9DBE31870F1A88A1 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.74;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
DB 154 LTRKXSP 161

```

RESULT 5
ID 014607 PRELIMINARY; PRT; 189 AA.
AC 014607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE INTERFERON-ALPHA-J1 (IFN-ALPHA-J1).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86005847; PubMed=2995168;
RA Cohen S., Velan B., Grosfeld H., Shalita Z., Leitner M.,
RA Shalerman A.;
RT "Cloning, expression and biological activity of a new variant of human
interferon alpha identified in virus induced lymphoblastoid cells.";
Dev. Biol. 60:111-122(1985).
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC EMBL; M34913; AAA36039.1; -.
DR HSSP; P01563; 2HE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SO SEQUENCE 189 AA; 22048 MW; 2AF6F48447BB72B3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 42; DB 4; Length 189;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8
Db 154 LTERKXSP 161

RESULT 6
ID 09N106 PRELIMINARY; PRT; 108 AA.
AC 09N106;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE INTERFERON ALPHA-1 (FRAGMENT).
GN IFN1A.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shine Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1246(1999).
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC EMBL; AF135017; AAF29603.1; -.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.

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DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12420 MW; 028CA54FFA97FACD CRC64;

Query Match
Best Local Similarity 85.7%; Score 36; DB 6; Length 108;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8
Db 95 LOEKXSP 102

RESULT 7
ID 029114 PRELIMINARY; PRT; 170 AA.
AC 029114;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE SHORT TYPE I INTERFERON PRECURSOR.
GN SPI IFN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);
RX MEDLINE=93374975; PubMed=7690039;
RA Lefevre F., Boulay V.;
RT "A novel and atypical type one interferon gene expressed by
trophoblast during early pregnancy.";
J. Biol. Chem. 268:19760-19768(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);
RX MEDLINE=86232600; PubMed=3714490;
RA von Heijne G.;
RT "A new method for predicting signal sequence cleavage sites.";
Nucleic Acids Res. 14:4683-4690(1986).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC EMBL; Z22706; CAAB0407.1; -.
DR HSSP; P01563; 1ITE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1
FT CHAIN 22 170 POTENTIAL.
FT VARIANT 88 88 S -> G.
FT VARIANT 101 101 N -> T.
SQ SEQUENCE 170 AA; 19906 MW; FEDI95EAFDD99AAB CRC64;

Query Match
Best Local Similarity 85.7%; Score 36; DB 6; Length 170;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8
Db 146 LTERKXSP 153

RESULT 8
Q29115

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ID 029115 PRELIMINARY; PRT; 170 AA.
AC 029115;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SHORT TYPE I INTERFERON PRECURSOR.
GN SPT IEN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX MEDLINE=86232600; PubMed=3714490;
RA von Heijne G.;
RT "A new method for predicting signal sequence cleavage sites.";
RL Nucleic Acids Res. 14:4683-4690(1986).
[1]
[2]
[3]
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX MEDLINE=87174805; PubMed=3550702;
RA Slinger D.S., Parent L.J., Ehrlich R.;
RT "Identification and DNA sequence of an interspersed repetitive DNA element in the genome of the miniature swine.";
RL Nucleic Acids Res. 15:2780-2780(1987).
[1]
[2]
[3]
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX MEDLINE=93374975; PubMed=7690039;
RA Lefevre F., Boulay V.;
RT "A novel and atypical type one interferon gene expressed by trophoblast during early pregnancy.";
RL J. Biol. Chem. 268:19760-19768(1993).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.
DR EMBL: Z22707; CAAB0408.1; -.
DR HSSP: P01563; IYF.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B-D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 170 SHORT TYPE I INTERFERON.
FT SEQUENCE 170 AA; 19863 MW; 563F7D2AE716AF51 CRC64;
Query Match 85.7%; Score 36; DB 6; Length 170;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 LTERKYS 8
DB 146 LKERKYS 153

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RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,
RA Tortum M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
RA Howm B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC T24D18 from Arabidopsis thaliana chromosome 1.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[1]
[2]
[3]
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[1]
[2]
[3]
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AC010924; AAF18507.1; -.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actite.
DR Pfam: PF00069; PKinase; 1.
DR SMART: SM00221; STYKC; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 730 AA; 81210 MW; B51DB48D95C73B5 CRC64;

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OY 1 LTERKYS 8
DB 224 LTKRYS 231
Query Match 85.7%; Score 36; DB 10; Length 730;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 LTERKYS 8
DB 224 LTKRYS 231
RESULT 10
ID 013619 PRELIMINARY; PRT; 181 AA.
AC 013619;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE P1028 PROTEIN (HYPOTHETICAL 20.3 KDA PROTEIN).
GN P1028 OR SPBP22H7.03.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=972 H-;
RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Halkawa Y., Yamazaki J.,
RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA Ogura K., Otsuka R., Kudo Y., Yanagida M., Machida M., Zhang M.Q.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[1]
[2]
[3]
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB004535; BAA21407.1; -.
DR EMBL: AL590883; CAC37371.1; -.
KW Hypothetical protein.
SEQUENCE 181 AA; 20293 MW; 2D6A1B61F0FD51B8 CRC64;

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Query Match 81.0%; Score 34; DB 3; Length 181;  
 Best Local Similarity 85.7%; Pred. No. 30;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKRYSP 8  
 :|||||  
 DB 70 SEKKYSP 76

RESULT 11

ID 035995 PRELIMINARY; PRT; 577 AA.  
 AC 035995;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MITOCHONDRIAL HSP70 HOMOLOG.  
 OC Vairimorpha necatrix.  
 OC Eukaryota; Microsporidia; Burenellidae; Vairimorpha.  
 NCBI\_TaxId=6039;  
 [1]  
 RC SEQUENCE FROM N.A.  
 AC TISSUE-SPORES;  
 AC Hirt R.P., Healy B., Vossbrinck C.R., Canning E.U., Embley T.M.;  
 RL Curr. Biol. 7:0-0(1997).  
 RL EMBL: AF008215; AAB81494.1; -  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PR00012; HSP70; 1.  
 DR PROSITE: PS00287; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR SEQUENCE 577 AA; 64744 MW; C649B069A94DDB8 CRC64;

Query Match 81.0%; Score 34; DB 5; Length 577;  
 Best Local Similarity 75.0%; Pred. No. 91;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTEKKYSP 8  
 :|||||  
 DB 110 IDEKKYSP 117

RESULT 12  
 Q9V6S9 PRELIMINARY; PRT; 1154 AA.  
 AC Q9V6S9;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE C618368 PROTEIN.  
 GN CG18368.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxId=7227;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRATIN-BERKELEY;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Gentler A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Malsbina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy E., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003817; AAF58343.1; -  
 DR FlyBase: FBgn0033864; CG18368.  
 DR SEQUENCE 1154 AA; 134414 MW; A1985DEBF780A01BA CRC64;

Query Match 81.0%; Score 34; DB 5; Length 1154;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKRYSP 8  
 :|||||  
 DB 166 TKRYSP 172

RESULT 13  
 ID Q9SY5 PRELIMINARY; PRT; 110 AA.  
 AC Q9SY5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE HYPOTHETICAL 13.2 KDA PROTEIN.  
 GN C7A10.800 OR A14G36560.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eurosids II; Brassicales; Brassicaceae; Arabidops's.  
 NCBI\_TaxId=3702;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Bevan M., Terry N., Vos P., Heljnen L., Mewes F.W., Mayer K.F.X.,  
 RA Schueller C.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z99708; CAB1637.1; -  
 DR EMBL: AL161589; CAB80322.1; -  
 KW Hypothetical protein.  
 SO SEQUENCE 110 AA; 13189 MW; 82DA67BF97311BA8 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 33; DB 10; Length 110;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
DB 36 EKKYSP 41

## RESULT 14

Q9CKT2 PRELIMINARY; PRT; 334 AA.  
AC Q9CKT2;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
GN HPA.  
OS HPA OR PM1524.  
SS Pasteurella multocida.  
CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Pasteurella.  
NCBI\_TaxID=747;  
OX  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM70;  
RX MEDLINE=21145866; PubMed=11248100;  
RA May B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;  
RT "Complete genomic sequence of Pasteurella multocida Fm70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
CC -1- SIMILARITY: BELONGS TO THE ARAC/XLYS FAMILY OF TRANSCRIPTIONAL REGULATORS.  
DR EMBL: AE006189; AK03608.1; -  
DR InterPro: IPR000005; HTHARAC.  
DR Pfam: PF00165; HTH\_ARAC.1.  
DR PRINTS: PR00032; HTHARAC.  
DR SMART: SM00342; HTH\_ARAC.1.  
DR PROSITE: PS00041; HTH\_ARAC\_FAMILY\_1; UNKNOWN\_1.  
DR PROSITE: PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
KM Complete proteome; DNA-binding; Transcription regulation.  
SQ SEQUENCE 334 AA; 39714 MW; 8532929C52246503 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 33; DB 2; Length 334;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
DB 214 EKKYSP 219

RESULT 15  
Q9WTU7 PRELIMINARY; PRT; 767 AA.  
AC Q9WTU7;  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE APOPTOSIS-LINKED PROTEIN 4, DELTAC FORM (FRAGMENT).  
GN PCDD1 OR ALG-4.  
OS Mus musculus (Mouse).  
SS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Memellia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
OX  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99244237; PubMed=10229231;  
RA Lacana' E., D'Adamo L.;  
RT "Regulation of fas ligand expression and cell death by apoptosis-linked gene 4.";  
RL Nat. Med. 5:542-547(1999).  
DR EMBL: AF055668; AAD20941.1; -  
DR HSP: P05055; ISRO.

DR MGD: MGI:1341788; Pcdcl1.  
DR InterPro: IPR000110; Ribosomal\_S1.  
DR InterPro: IPR003029; S1.  
DR Pfam: PF00575; S1; 4.  
DR PRINTS: PR00681; RIBOSOMALS1.  
DR SMART: SM00316; S1; 6.  
FT NON\_TER 1  
FT NON\_TER 767  
SQ SEQUENCE 767 AA; 84512 MW; 81B692B073E697FA CRC64;

Query Match  
Best Local Similarity 100.0%; Score 33; DB 11; Length 767;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
DB 101 EKKYSP 106

RESULT 16  
Q9V8W6 PRELIMINARY; PRT; 83 AA.  
AC Q9V8W6;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
DE CG16926 PROTEIN.  
GN Drosophila melanogaster (Fruit fly).  
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; CC Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
OX  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunn P., Durbin K.J., Evangelista C.C., Ferriaz C., Ferrieres M., Fleischmann W., Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegwu C., Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector A.C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 Science 287:2185-2195(2000).  
 DR EMBL; AE003750; AAF56387.1;  
 DR FlyBase; FBgn0040732; CG16926.  
 SO SEQUENCE 83 AA; 9420 MW; 4A99D5F8BC2B680 CRC64;

Query Match 76.2%; Score 32; DB 5; Length 83;  
 Best Local Similarity 62.5%; Pred. No. 35;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
 Db 44 LTRKXSP 51

RESULT 17  
 ID 09VBY9 PRELIMINARY; PRT; 400 AA.  
 AC 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CG13649 PROTEIN.  
 GN CG13649.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydrozoa; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid=7227;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Ramanakides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang L.X.,  
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Miklos G.L.G.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfister B.D.,  
 Adill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,  
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Doudon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 Jaitani M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacלב J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 SO Science 287:2185-2195(2000).

DR EMBL; AE003750; AAF56387.1;  
 DR FlyBase; FBgn0039267; CG13649.  
 DR InterPro; IPR003889; FYRICH\_C.  
 DR InterPro; IPR003888; FYRICH\_N.  
 DR SMART; SM00542; FYRC; 1.  
 DR SMART; SM00541; FYRN; 1.  
 SO SEQUENCE 400 AA; 45117 MW; 71CA68BD650E3F CRC64;

Query Match 76.2%; Score 32; DB 5; Length 400;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTKXSP 8  
 Db 77 TTKXSP 83

RESULT 18  
 ID 09SX74 PRELIMINARY; PRT; 414 AA.  
 AC 09SX74;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE F11A17.2 PROTEIN (TIN15.3).  
 GN F11A17.2.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_Taxid=3702;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Vysotskaya V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,  
 Lee J.M., Li J., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M.,  
 Sakano H., Chinn C., Choi E., Chou J., Altati H., Araujo R.,  
 Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Dunn P.,  
 Hansen N., Hwang B., Huizar L., Khan S., Kim C., Palm C., Rowley D.,  
 Shin P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A.,  
 Theologis A.;  
 RT "thaliana chloroplast genome 1 BAC F11A17 sequence."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,  
 Shin P., Altati H., Bei Q., Chinn C., Chou J., Choi E., Conn L.,  
 Conway A., Gonzales A., Hansen N., Hwang B., Koo T., Lam B., Lee J.,  
 Lenz C., Li J., Liu A., Liu K., Liu S., Mukharly N., Nguyen M.,  
 Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
 Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 Ecker J.R.;  
 RT "Genomic sequence for Arabidopsis thaliana BAC TIN15 from chromosome 1."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RC SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RC SEQUENCE FROM N.A.  
 RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 Khan S., Kim C., Altati H., Bei B., Chinn C., Chou J., Choi E.,  
 Conn L., Conway A., Gonzales A., Hansen N., Hwang B., Koo T., Lam B.,  
 Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharly N.,  
 Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 Theologis A., Ecker J.R.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC007932; AAD49754.2; -  
 DR EMBL: AC020889; AAF79717.1; -  
 DR InterPro: IPR001926; PALP.  
 SO SEQUENCE 414 AA; 45332 MW; 2793ED5661D95DD5 CRC64;

Query Match 76.2%; Score 32; DB 10; Length 414;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 DB 32 LTERKYS 39

RESULT 19  
 Q23323 PRELIMINARY; PRT; 573 AA.

Q23323; 01-NOV-1996 (TREMREL. 01, Created)  
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)  
 DE ZC443.5 PROTEIN.  
 CN ZC443.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;  
 OC Rhabditiidae; Peloderiinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Baynes C.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Lettelle P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Showkeen R.,  
 RA Smailson N., Smith A., Sonnenhammer E., Staden R., Sulston J.,  
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: Z75553; CAA89950.1;  
 DR InterPro: IPR002213; UDPGT.  
 DR Pfam: PF00201; UDPGT.1.  
 SO SEQUENCE 573 AA; 65645 MW; 5429DJ3388BCH40F CRC64;

Query Match 76.2%; Score 32; DB 5; Length 573;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYS 7  
 DB 475 LTERKYS 481

RESULT 20

ID 095022 PRELIMINARY; PRT; 1528 AA.

AC 095022;  
 DT 01-FEB-1997 (TREMREL. 02, Created)  
 DT 01-FEB-1997 (TREMREL. 02, Last sequence update)  
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)  
 DE P-ATPASE.  
 GN CPAA-El.

OS Cryptosporidium parvum.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 OC Cryptosporidiidae; Cryptosporidium.  
 OC NCBI\_TaxID=5807;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=KSU-1.  
 RA Zhu G., Khrantsov N., Upton S.J., Keithly J.S.;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U65981; AAC47833.1; -  
 DR HSSP: P04191; IEUL.  
 DR InterPro: IPR001757; E1-E2\_ATPase.  
 DR InterPro: IPR001454; Hydrolyase.  
 DR Pfam: PF00122; E1-E2\_ATPase.  
 DR Pfam: PF00702; Hydrolyase; 1.  
 DR PRINTS: PR00119; CATAPASE.  
 DR PROSITE: PS00154; ATPASE\_E1\_E2; UNKNOWN\_1.  
 KW Hydrolyase.  
 SO SEQUENCE 1528 AA; 168873 MW; 82AECB973C207D8B CRC64;

Query Match 76.2%; Score 32; DB 5; Length 1528;  
 Best Local Similarity 75.0%; Pred. No. 5.9e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 DB 242 LTERKYS 249

RESULT 21

ID 091E09 PRELIMINARY; PRT; 60 AA.

AC 091E09;  
 DT 01-OCT-2000 (TREMREL. 15, Created)  
 DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)  
 DE AV2 PROTEIN (FRAGMENT).  
 GN AV2.  
 OS cotton leaf curl virus.  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OC NCBI\_TaxID=53010;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B27-IR.  
 RX MEDLINE=20318672; PubMed=10859391;  
 RA Sanz A.T., Fralle A., Garcia-Arenal F., Zhou X., Robinson D.J.,  
 RA Khalid S., Butt T., Harrison B.D.;  
 RT "Multiple infection, recombination and genome relationships among  
 RT begomovirus isolates found in cotton and other plants in Pakistan.";  
 RL J. Gen. Virol. 81:1839-1849(2000).  
 DR EMBL: AJ270861; CAB97098.1;  
 DR InterPro: IPR002511; GeminV\_VI.  
 DR Pfam: PF01524; GeminV\_VI.  
 DR ProDom: PD002978; GeminV\_VI; 1.  
 FT NON\_TER 60  
 SO SEQUENCE 60 AA; 7035 MW; 113D7E8980D7EFBC CRC64;

Query Match 73.8%; Score 31; DB 12; Length 60;  
 Best Local Similarity 75.0%; Pred. No. 41;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 DB 27 LTERKYS 34

RESULT 22

ID 09F554 PRELIMINARY; PRT; 113 AA.

AC 09F554;  
 DT 01-MAR-2001 (TREMREL. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)  
 DE RELAXOSOME COMPONENT.  
 GN NTKA.  
 OS Escherichia coli.  
 OC Plasmid R721.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia  
 NCBI\_TaxID=562;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12; TRANSPOSON-TN7;  
 RA Samped G., Motomura K., Masuda S., Yamaguchi T., Ando K., Oishi T.,  
 RA Puriya N., Komano T., Mizobuchi K.;  
 RT "Organization and diversification of plasmid genomes: complete  
 RT nucleotide sequence of the R721 genome."  
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.  
 RN (12)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12; TRANSPOSON-TN7;  
 MEDLINE=93015772; PubMed=1400257;  
 Kim S., Komano T.;  
 "Nucleotide sequence of the R721 shuffleon."  
 J. Bacteriol. 174:7053-7058(1992).  
 DR EMBL: AP002527; BAB12623.1;  
 DR InterPro: IPR002145; COPG\_HTH\_4.  
 DR Pfam: PF01402; HTH\_4; 1.  
 KW Plasmid.  
 SQ SEQUENCE 113 AA; 13147 MW; C7D3B2406A25DA9C CRC64;

Query Match 73.8%; Score 31; DB 2; Length 113;  
 Best Local Similarity 62.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 |||::|  
 Db 15 LTEREYAP 22

RESULT 23  
 ID 088551 PRELIMINARY; PRT; 118 AA.  
 AC 088551;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)  
 DE PRECOAT PROTEIN.  
 GN V2.  
 OS Tomato yellow leaf curl virus (TYLCV).  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 NCBI\_TaxID=10832;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BANGALORE II, INDIA;  
 RA Chatchawanphanich O., Chiang B.T., Green S.K., Singh S.J.,  
 RA Mehta P., Maxwell D.P.;  
 RT Submitted (Oct-1995) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U38239; AAB08928.1;  
 DR InterPro: IPR002511; Geminl\_VL.  
 DR Pfam: PF01524; Geminl\_VL; 1.  
 DR ProDom: PD002978; Geminl\_VL; 1.  
 KW Coat protein.  
 SQ SEQUENCE 118 AA; 13724 MW; 89E41A39BF7FF6B3 CRC64;

Query Match 73.8%; Score 31; DB 12; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 79;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 |||  
 Db 27 LVEKTYSP 34

RESULT 24  
 ID 073583 PRELIMINARY; PRT; 118 AA.  
 AC 073583;  
 DT 01-AUG-1998 (TREMblrel. 07, Created)  
 DT 01-AUG-1998 (TREMblrel. 07, last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)  
 DE AV2 PROTEIN.  
 GN AV2.  
 OS cotton leaf curl virus.  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 NCBI\_TaxID=53010;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PAKISTAN;  
 RX MEDLINE=98227943; PubMed=9568988;  
 RA Zhou X., Liu Y., Robinson D.J., Harrison B.D.;  
 RT "Four DNA-A variants among Pakistani isolates of cotton leaf curl  
 RT virus and their affinities to DNA-A of geminivirus isolates from  
 RT okra."  
 RL J. Gen. Virol. 79:915-923(1998).  
 DR EMBL: A002449; CA05432.1;  
 DR EMBL: A002448; CA05426.1;  
 DR InterPro: IPR002511; Geminl\_VL.  
 DR Pfam: PF01524; Geminl\_VL; 1.  
 DR ProDom: PD002978; Geminl\_VL; 1.  
 SQ SEQUENCE 118 AA; 13721 MW; 72948EF3538BA408 CRC64;

Query Match 73.8%; Score 31; DB 12; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 79;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 |||  
 Db 27 LVEKTYSP 34

RESULT 25  
 ID 090DE8 PRELIMINARY; PRT; 118 AA.  
 AC 090DE8;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)  
 DE PRE-COAT PROTEIN.  
 GN V2.  
 OS tomato leaf curl geminivirus.  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 NCBI\_TaxID=28350;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TLCV-BD2;  
 RA Shih S.L., Tsai W.S., Nakha M.K., Maxwell D.P., Rashid M.H.,  
 RA Green S.K.;  
 RT "Molecular comparison of two tomato leaf curl viruses from  
 RT Bangladesh."  
 RL Zhifu Baohuixue Hui Huihan 40:436-437(1998).  
 RN (12)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TLCV-BD2;  
 RA Tsai W.S., Nakha M.K., Maxwell D.P., Rashid M.H., Green S.K.;  
 RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF168481; AAF04835.1;  
 DR InterPro: IPR002511; Geminl\_VL.  
 DR Pfam: PF01524; Geminl\_VL; 1.  
 DR ProDom: PD002978; Geminl\_VL; 1.  
 KW Coat protein.  
 SQ SEQUENCE 118 AA; 13704 MW; FD978795A13FE443 CRC64;

Query Match 73.8%; Score 31; DB 12; Length 118;  
Best Local Similarity 75.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
| | | | |  
Db 27 LVEKTYSP 34

Search completed: January 15, 2002, 08:45:34  
Job time: 300 sec

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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:40:04 ; Search time 12.84 Seconds  
(without alignments)  
22.844 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LTERKXSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	189	1	INA1_HUMAN
2	42	100.0	189	1	INA4_HUMAN
3	42	100.0	189	1	INA5_HUMAN
4	42	100.0	189	1	INA6_HUMAN
5	42	100.0	189	1	INA7_HUMAN
6	42	100.0	189	1	INA8_HUMAN
7	36	85.7	184	1	INA1_HORSE
8	36	85.7	184	1	INA2_HORSE
9	36	85.7	184	1	INA3_HORSE
10	36	85.7	184	1	INA4_HORSE
11	36	85.7	188	1	INA2_HUMAN
12	36	85.7	189	1	INA7_HUMAN
13	36	85.7	189	1	INA7_HUMAN
14	36	85.7	194	1	INA_FELCA
15	35	83.3	189	1	INA8_HUMAN
16	35	83.3	195	1	INO1_HORSE
17	34	81.0	528	1	LAD1_MOUSE
18	33	78.6	189	1	INA4_HUMAN
19	32	76.2	114	1	FVE_FLAIVE
20	31	73.8	189	1	INA1_MOUSE
21	31	73.8	189	1	INA1_PIG
22	31	73.8	189	1	INA5_MOUSE
23	31	73.8	189	1	INA6_MOUSE
24	31	73.8	189	1	INA8_MOUSE
25	31	73.8	190	1	INA2_MOUSE
26	31	73.8	190	1	INA7_MOUSE
27	31	73.8	195	1	INA9_MOUSE
28	31	73.8	270	1	BLOC_PSEAR
29	31	73.8	545	1	FLIF_BUCAL
30	31	73.8	779	1	ZW10_HUMAN
31	31	73.8	959	1	NI00_YEAST
32	30	71.4	229	1	CSE4_YEAST
33	30	71.4	270	1	TPIS_CHLMO

## ALIGNMENTS

RESULT	1	STANDARD	PRT	189	AA
INA1_HUMAN					
ID	INA1_HUMAN				
AC	P01562				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (IEIF D).				
GN	IFNA1 AND IFNA13.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81005094; PubMed=6157600;				
RA	Mantel N., Schwarstein M., Streull M., Panem S., Nagata S., Weissmann C.;				
RT	"The nucleotide sequence of a cloned human leukocyte interferon cDNA."				
RL	Gene 10:1-10(1980).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=80254543; PubMed=6157095;				
RA	Taniguchi T., Mantel N., Schwarstein M., Nagata S., Muramatsu M., Weissmann C.;				
RT	"Human leukocyte and fibroblast interferons are structurally related."				
RL	Nature 285:547-549(1980).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81148795; PubMed=6163083;				
RA	Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M., McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;				
RT	"The structure of eight distinct cloned human leukocyte interferon cDNAs."				
RL	Nature 290:20-26(1981).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85003592; PubMed=6479148;				
RA	Todoroko K., Kiousis D., Weissmann C.;				
RT	"Two non-allelic human interferon alpha genes with identical coding regions."				
RL	EMBO J. 3:1809-1812(1984).				
CC	-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.				
CC	-1- MISCELLANEOUS: INTERFERONS ALPHA-1 AND ALPHA-13 HAVE IDENTICAL PROTEIN SEQUENCES.				
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.				

34	30	71.4	373	1	Y085_METUA	057550 methanococ
35	30	71.4	383	1	C057_YEAST	Q07788 saccharomyc
36	30	71.4	726	1	NU84_YEAST	P52891 saccharomyc
37	30	71.4	879	1	DPOL_WHV1	P03160 woodchuck h
38	30	71.4	883	1	DPOL_WHV8	P06275 woodchuck h
39	30	71.4	884	1	DPOL_WHV7	P12898 woodchuck h
40	30	71.4	884	1	DPOL_WHV8	P17396 woodchuck h
41	30	71.4	1294	1	RPOB_WCMVO	P15402 white clove
42	30	71.4	1391	1	RPOB_MYCPN	P78013 mycoplasma
43	29	69.0	189	1	INAF_HUMAN	P05015 homo sapien
44	29	69.0	195	1	INO2_HUMAN	P05002 homo sapien
45	29	69.0	195	1	INO2_HORSE	P05002 equus cabal
46	29	69.0	195	1	INT_GIRCA	Q95187 girafa cam
47	29	69.0	209	1	RANA_LOTJA	P54765 lotus japon
48	29	69.0	209	1	RANA_LOTJA	P54766 lotus japon
49	29	69.0	217	1	FRAL_VIBFI	P46072 vibrio fisc
50	29	69.0	221	1	RAN_VICFA	P38548 vicia faba

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-----  
DR EMBL: J00210; AAB59403.1; -  
DR EMBL: V00537; CAA23798.1; -  
DR EMBL: V00538; CAA23799.1; -  
DR EMBL: X00803; CAA23581.1; -  
DR PIR: A01826; IYH0A1.  
DR PIR: C23285; C23285.  
DR HSSP: P01563; 2HTE.  
DR MIM: 147578; -  
DR MIM: 147660; -  
DR InterPro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon; 1.  
DR PRINTS: PR00266; INTERFERONAB.  
DR ProDom: PD000550; Interferon\_abd; 1.  
DR SMART: SM00076; IFabd; 1.  
DR PROSITE: PS00252; INTERFERON\_A\_B\_D; 1.  
DR Cytokine; Antiviral; Multigene family; Signal.  
KW SIGNAL 1 23  
FT CHAIN 24 189 INTERFERON ALPHA-1/13.  
FT DISULFID 24 122 BY SIMILARITY.  
FT DISULFID 52 162 BY SIMILARITY.  
FT CONFLICT 137 137 A -> V (IN REF. 3).  
SQ SEQUENCE 189 AA; 21725 MW; F32F9CB969606B69 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
INAA\_HUMAN  
AC P05014; P13358; STANDARD; PRT; 189 AA.  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE INTERFERON ALPHA-4 PRECURSOR (INTERFERON ALPHA-4B) (INTERFERON  
DE ALPHA-M1) (INTERFERON ALPHA-76).  
GN IFNA4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86037205; PubMed=4057246;  
RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,  
RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;  
RT "Structural relationship of human interferon alpha genes and  
RT pseudogenes";  
RL J. Mol. Biol. 185:227-260(1985).  
[2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=84307815; PubMed=6089830;  
RA Linnane A.W., Belharz M.W., McMullen G.L., Macreadie I.G.,  
RA Murphy M., Nisbet I.T., Novitski C.E., Woodrow G.C.;  
RT "Nucleotide sequence and expression in E. coli of a human interferon-  
RT alpha gene selected from a genomic library using synthetic  
RT oligonucleotides";

RL Biochem. Int. 8:725-732(1984).  
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.  
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-----  
DR EMBL: X02955; CAA26701.1; -  
DR EMBL: M27318; AAB52726.1; -  
DR PIR: E23753; IYH04B.  
DR HSSP: P01563; 1ITF.  
DR MIM: 147564; -  
DR InterPro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon; 1.  
DR PRINTS: PR00266; INTERFERONAB.  
DR ProDom: PD000550; Interferon\_abd; 1.  
DR SMART: SM00076; IFabd; 1.  
DR PROSITE: PS00252; INTERFERON\_A\_B\_D; 1.  
DR Cytokine; Antiviral; Multigene family; Signal.  
KW SIGNAL 1 23  
FT CHAIN 24 189 INTERFERON ALPHA-4.  
FT DISULFID 24 122 BY SIMILARITY.  
FT DISULFID 52 162 BY SIMILARITY.  
FT CONFLICT 74 74 T -> A (IN REF. 2).  
FT CONFLICT 137 137 V -> E (IN REF. 2).  
SQ SEQUENCE 189 AA; 21808 MW; 4198F9CC8E2A80C CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
INAA\_HUMAN  
AC P01569; STANDARD; PRT; 189 AA.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE INTERFERON ALPHA-5 PRECURSOR (INTERFERON ALPHA-G) (LEIF G) (INTERFERON  
DE ALPHA-61).  
GN IFNA5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86037205; PubMed=4057246;  
RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,  
RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;  
RT "Structural relationship of human interferon alpha genes and  
RT pseudogenes";  
RL J. Mol. Biol. 185:227-260(1985).  
[2]  
RN SEQUENCE OF 57-189 FROM N.A.  
RX TISSUE=Spleen;  
RX MEDLINE=81148795; PubMed=6163083;  
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,



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RA McDaniel R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte interferon
RL cDNAs."
CC Nature 290:20-26(1991).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
CC EMBL: X02956; CAA26702.1; -.
CC EMBL: V00541; CAA23802.1; -.
CC PIR: A01833; IYHU07.
CC HSSP: P01563; 2HIE.
CC MIM: 147565; -.
CC InterPro: IPR000471; Interferon_abd.
CC Pfam: PF00143; Interferon_1.
CC PRINTS: PR00266; INTERFERONAB.
CC PRODOM: PD000550; Interferon_abd; 1.
CC SMART: SM00076; IFabd; 1.
CC PROSITE: PS00252; INTERFERON_A-B-D; 1.
CC DR SMART; SM00076; IFabd; 1.
CC KW Cytokine; Antiviral; Multigene family; Signal.
CC FT CHAIN 1 23
CC FT SIGNAL 1 23
CC FT DISULFID 24 189 INTERFERON ALPHA-5.
CC FT DISULFID 24 122 BY SIMILARITY.
CC FT DISULFID 52 162 BY SIMILARITY.
CC SEQUENCE 189 AA; 21942 MW; C605992FE2E78043 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEEKKXSP 8
DB 154 LEEKKXSP 161

RESULT 4
INAG_HUMAN STANDARD; PRT; 189 AA.
P05013;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-6 PRECURSOR (INTERFERON ALPHA-K) (LEIF K) (INTERFERON
DE ALPHA-54).
GN IFNA6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86037205; PubMed=4057246;
RA Henco K., Brosius J., Fujisawa J.-I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasak M., Schambeck A., Schmid J.,
RA Todokoro K., Maechli M., Nagata S., Weissmann C.;
RT "Structural relationship of human Interferon alpha genes and
RT pseudogenes."
RL J. Mol. Biol. 185:227-260(1985).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA

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CC -----
CC EMBL: X02958; CAA26704.1; -.
CC PIR: A23753; IYHU16.
CC HSSP: P01563; 1IYF.
CC MIM: 147566; -.
CC InterPro: IPR000471; Interferon_abd.
CC Pfam: PF00143; Interferon_1.
CC PRINTS: PR00266; INTERFERONAB.
CC PRODOM: PD000550; Interferon_abd; 1.
CC DR SMART; SM00076; IFabd; 1.
CC DR PROSITE; PS00252; INTERFERON_A-B-D; 1.
CC KW Cytokine; Antiviral; Multigene family; Signal.
CC FT CHAIN 1 23
CC FT SIGNAL 1 23
CC FT DISULFID 24 189 INTERFERON ALPHA-6.
CC FT DISULFID 24 122 BY SIMILARITY.
CC FT DISULFID 52 162 BY SIMILARITY.
CC SEQUENCE 189 AA; 22140 MW; 8C7F3F90F12C562E CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEEKKXSP 8
DB 154 LEEKKXSP 161

RESULT 5
INAG_HUMAN STANDARD; PRT; 189 AA.
AC P01571;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-17 PRECURSOR (INTERFERON ALPHA-I') (INTERFERON
DE ALPHA-T) (INTERFERON ALPHA-88).
GN IFNA17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81201124; PubMed=6165082;
RA Lavin R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;
RT "DNA sequence of two closely linked human leukocyte Interferon
RT genes."
RL Science 212:1159-1162(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85229953; PubMed=3891272;
RA Mizoguchi J., Pitha P.M., Raj N.B.K.;
RT "Efficient expression in Escherichia coli of two species of human
RT interferon-alpha and their hybrid molecules."
RL DNA 4:221-232(1985).
RN [3]
RP SEQUENCE OF 14-189 FROM N.A.
RX MEDLINE=85235859; PubMed=4008999;
RA Lund B., von Gabain A., Edlund T., Ny T., Lundgren E.;
RT "Differential expression of interferon genes in a substrain of
RT Namalwa cells."
RL J. Interferon Res. 5:229-238(1985).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL

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CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGADENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 CC DR EMBL: M1026; AAA52725.1; -  
 CC DR EMBL: V00532; CAA23793.1; -  
 CC DR EMBL: M71246; AAA52713.1; -  
 CC DR PIR: A01835; IVHUA9.  
 CC DR PIR: A22255; A22255.  
 CC DR HSSP: P01563; 1TFE.  
 CC DR MIM: 147583; -  
 CC DR InterPro: IPR000471; Interferon\_abd.  
 CC DR Pfam: PF00143; Interferon; 1.  
 CC DR PRINTS: PR00266; INTERFERONAB.  
 CC DR ProDom: PD000550; Interferon\_abd; 1.  
 CC DR SMART: SM00076; IFab; 1.  
 CC DR PROSITE: PS00252; INTERFERON\_A\_B\_D; 1.  
 CC DR CYTOKINE; Antiviral; Multigene family; Signal.  
 CC FT SIGNAL 1 23  
 CC FT CHAIN 1 189  
 CC FT DISULFID 24 122 BY SIMILARITY.  
 CC FT DISULFID 52 162 BY SIMILARITY.  
 CC FT CONFLICT 57 57 H -> P (IN REF. 1).  
 CC FT CONFLICT 184 184 I -> R (IN REF. 3).  
 CC FT SEQUENCE 189 AA; 21728 MW; 0448EAB9D7FC32 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYP 8  
 DB 154 LTERKYP 161

RL DOK1. Biochem. 269:91-95(1983).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES. IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGADENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 CC DR EMBL: M12350; AAA52718.1; -  
 CC DR EMBL: V00340; CAA23801.1; -  
 CC DR EMBL: X00145; CAA24980.1; -  
 CC DR PIR: A01832; IVHUF.  
 CC DR HSSP: P01563; 2HIE.  
 CC DR MIM: 147584; -  
 CC DR InterPro: IPR000471; Interferon\_abd.  
 CC DR Pfam: PF00143; Interferon; 1.  
 CC DR PRINTS: PR00266; INTERFERONAB.  
 CC DR ProDom: PD000550; Interferon\_abd; 1.  
 CC DR SMART: SM00076; IFab; 1.  
 CC DR PROSITE: PS00252; INTERFERON\_A\_B\_D; 1.  
 CC DR CYTOKINE; Antiviral; Multigene family; Signal.  
 CC FT SIGNAL 1 23  
 CC FT CHAIN 1 189  
 CC FT DISULFID 24 122 BY SIMILARITY.  
 CC FT DISULFID 52 162 BY SIMILARITY.  
 CC FT CONFLICT 119 119 M -> L (IN REF. 2).  
 CC FT SEQUENCE 189 AA; 21759 MW; 05B7BD86929059B3 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYP 8  
 DB 154 LTERKYP 161

RESULT 6  
 INAK\_HUMAN STANDARD; PRT; 189 AA.  
 AC P01568;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-21 PRECURSOR (INTERFERON ALPHA-F) (LEIF F).  
 GN IFNA21.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gren E.Y., Berzin V.M., Tsimanis A.Y., Apsalon U.R., Vishnevskii Y.I.,  
 RA Yansore I.V., Dishler A.V., Pudova N.V., Smorodintsev A.A.,  
 RA Iovlev V.I., Stepanov A.N., Feldmane G.Y., Meldrals Y.A., Lozha V.P.,  
 RA Krasan V.M., Efimov V.A., Sverdlov E.D.;  
 RA "A new type of leukocytic interferon.";

RESULT 7  
 INAL\_HORSE STANDARD; PRT; 184 AA.  
 AC P05003;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE INTERFERON ALPHA-1 PRECURSOR.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Himmel A., Hauptmann R., Adolf G.R., Sweetly P.;  
 RA "Molecular cloning and expression in Escherichia coli of equine type  
 RA I interferon.";  
 RA DNA 5:345-356(1986).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGADENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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EMBL; M14540; AAA30953.1; -

DR PIR; A24912; IVHOA1.

DR HSSP; P01563; 2HIE.

DR InterPro: IPR000471; Interferon\_abd.

DR Pfam; PF00143; Interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR ProDom; PD000550; Interferon\_abd; 1.

DR SMART; SM00076; IFabd; 1.

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

FT SIGNAL 1 23

FT CHAIN 24 184 INTERFERON ALPHA-1.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SO SEQUENCE 184 AA; 20808 MW; 9E860B8CD05C83E6 CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;  
Best Local Similarity 87.5%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKXSP 8  
| | | | | | | |

Db 154 LOEKXSP 161

RESULT 8  
ID INA3\_HORSE STANDARD; PRT; 184 AA.

AC P05004;

DT 13-AUG-1987 (rel. 05, Created)

DT 13-AUG-1987 (rel. 05, Last sequence update)

DT 01-MAR-1989 (rel. 10, Last annotation update)

DE INTERFERON ALPHA-2 PRECURSOR.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_Taxid=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-87053170; PubMed-3022999;

RA Himmeler A., Hauptmann R., Adolf G.R., Swetly P.;  
"Molecular cloning and expression in Escherichia coli of equine type I interferons.";

RT DNA 5:345-356(1986).

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.

CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.

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EMBL; M14541; AAA30950.1; -

DR EMBL; A15987; CAA01258.1; -

DR PIR; B24912; IVHOA2.

DR HSSP; P01563; 2HIE.

DR InterPro: IPR000471; Interferon\_abd.

DR Pfam; PF00143; Interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR ProDom; PD000550; Interferon\_abd; 1.

DR SMART; SM00076; IFabd; 1.

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

FT SIGNAL 1 23

FT CHAIN 24 184 INTERFERON ALPHA-1.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SO SEQUENCE 184 AA; 20782 MW; 4C15D991ECA6D24A CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;  
Best Local Similarity 87.5%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

FT SIGNAL 1 23

FT CHAIN 24 184 INTERFERON ALPHA-2.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SO SEQUENCE 184 AA; 20877 MW; FC15DC7D811C68EC CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;  
Best Local Similarity 87.5%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKXSP 8  
| | | | | | | |

Db 154 LOEKXSP 161

RESULT 9  
ID INA3\_HORSE STANDARD; PRT; 184 AA.

AC P05005;

DT 13-AUG-1987 (rel. 05, Created)

DT 13-AUG-1987 (rel. 05, Last sequence update)

DT 01-MAR-1989 (rel. 10, Last annotation update)

DE INTERFERON ALPHA-3 PRECURSOR.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_Taxid=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-87053170; PubMed-3022999;

RA Himmeler A., Hauptmann R., Adolf G.R., Swetly P.;  
"Molecular cloning and expression in Escherichia coli of equine type I interferons.";

RT DNA 5:345-356(1986).

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.

CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.

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EMBL; M14542; AAA30951.1; -

DR EMBL; A16555; CAA01292.1; -

DR PIR; C24912; IVHOA3.

DR HSSP; P01563; 2HIE.

DR InterPro: IPR000471; Interferon\_abd.

DR Pfam; PF00143; Interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR ProDom; PD000550; Interferon\_abd; 1.

DR SMART; SM00076; IFabd; 1.

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

FT SIGNAL 1 23

FT CHAIN 24 184 INTERFERON ALPHA-3.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SO SEQUENCE 184 AA; 20782 MW; 4C15D991ECA6D24A CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;  
Best Local Similarity 87.5%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY      1 LTRKRYSP 8
DB      154 LOEKRYSP 161

RESULT 10
INNA_HORSE STANDARD; PRT; 184 AA.
AC P05006;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE INTERFERON ALPHA-4 PRECURSOR.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RT MEDLINE=87053170; PubMed=3022999;
NA Hummel A., Hauptmann R., Adolf G.R., Swelly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
RT I interferons".
RL DNA 5:345-356(1986).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M14543; AAA30952.1; -.
DR PIR; D24912; IVHOA4.
DR HSSP; P01563; IYTF.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Cytokine; Antiviral; Multigene family; Signal.
DR SIGNAL
FT CHAIN 1 23
FT DISULFID 24 184 INTERFERON ALPHA-4.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 184 AA; 20860 MW; FC087F46F11C6BEC CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 LTRKRYSP 8
DB      154 LOEKRYSP 161

RESULT 11
INNA_HUMAN STANDARD; PRT; 188 AA.
AC P01563; P01564; Q14606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-2 PRECURSOR (INTERFERON ALPHA-A) (LEIF A).
IFNA2.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT MEDLINE=81052322; PubMed=6159538;
RA Goeddel D.V., Yelverton E., Ullrich A., Heyneker H.L., Mizzari G.,
RA Holmes W., Seeburg P.H., Dull T.J., May L., Stebbins N., Crea R.,
RA Maeda S., McCandless R., Sloma A., Tabor J.M., Gross M.,
RA Familletti P.C., Pestka S.;
RT "Human leukocyte interferon produced by E. coli is biologically
RT active."
RL Nature 287:411-416(1980).
RN [2]
RP SEQUENCE FROM N.A.
RT MEDLINE=81148795; PubMed=6163083;
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte interferon
RT cDNAs."
RL Nature 290:20-26(1981).
RN [3]
RP SEQUENCE FROM N.A.
RT MEDLINE=82060261; PubMed=6170983;
RA Lawn R.M., Gross M., Houck C.M., Franke A.E., Gray P.V.,
RA Goeddel D.V.;
RT "DNA sequence of a major human leukocyte interferon gene."
RL Proc. Natl. Acad. Sci. U.S.A. 78:5435-5439(1981).
RN [4]
RP SEQUENCE FROM N.A.
RT TISSUE=Bone marrow tumor;
RP MEDLINE=66069501; PubMed=3906813;
RA Oliver G., Balbas P., Valle F., Soboron X., Bolivar F.;
RT "Cloning of human leukocyte interferon cDNA and a strategy for its
RT production in E. coli."
RL Rev. Latinoam. Microbiol. 27:141-150(1985).
RN [5]
RP SEQUENCE OF 7-188 FROM N.A.
RX MEDLINE=81015442; PubMed=6158094;
RA Streuli M., Nagata S., Weissmann C.;
RT "At least three human type alpha interferons: structure of alpha 2."
RL Science 209:1343-1347(1980).
RN [6]
RP SEQUENCE OF 24-188 FROM N.A.
RX MEDLINE=83299241; PubMed=6310510;
RA Weber H., Weissmann C.;
RT "Formation of genes coding for hybrid proteins by recombination
RT between related, cloned genes in E. coli."
RL Nucleic Acids Res. 11:5661-5669(1983).
RN [7]
RP SEQUENCE OF 24-112 AND 136-188.
RX MEDLINE=81052321; PubMed=6159537;
RA Allen G., Fantes K.H.;
RT "A family of structural genes for human lymphoblastoid
RT (leukocyte-type) interferon."
RL Nature 287:408-411(1980).
RN [8]
RP DISULFIDE BONDS.
RX MEDLINE=81123083; PubMed=6162107;
RA Wetzel R.;
RT "Assignment of the disulphide bonds of leukocyte interferon."
RL Nature 289:606-607(1981).
RN [9]
RP CARBOHYDRATE-LINKAGE SITE THR-129.
RX MEDLINE=91264809; PubMed=2049076;
RA Adolf G.R., Kalsner I., Ahorn H., Maurer Fogy I., Cantelli K.;
RT "Natural human interferon-alpha 2 is O-glycosylated."
RL Biochem. J. 276:511-518(1991).
RN [10]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=94052087; PubMed=8234245;
RA Murgolo N.J., Windsor W.T., Hruza A., Reichert P., Tsaropoulos A.,

```

RA Baldwin S., Huang E., Pramanik B., Ealick S., Trotta P.P.;  
 RT "A homology model of human interferon alpha-2.";  
 RL Proteins 17:62-74(1993).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE-97148339; PubMed-8994971;  
 RA Radhakrishnan R., Walter L.J., Hruza A., Reichert P., Trotta P.P.,  
 RT Nagabhushan T.L., Walter M.R.;  
 RT "Zinc mediated dimer of human interferon-alpha 2b revealed by X-ray  
 crystallography.";  
 RL Structure 4:1453-1463(1996).  
 RN [12]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-98118493; PubMed-9417943;  
 RA Klaus W., Gsell B., Labhardt A.M., Wipf B., Senn H.;  
 RT "The three-dimensional high resolution structure of human interferon  
 alpha-2a determined by heteronuclear NMR spectroscopy in solution.";  
 RL J. Mol. Biol. 274:661-675(1997).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, TEN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- POLYMORPHISM: TWO FORMS, ALPHA-2A AND ALPHA-2B DIFFER BY A SINGLE  
 CC RESIDUE (POSITION 46).  
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAMES ROBERON-A (ROCHE) OR  
 CC INTRON-A (SCHERING-PLOUGH). USED AS AN ANTICANCER DRUG FOR ITS  
 CC ANTIPROLIFERATIVE ACTIVITY.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 DR EMBL; J00207; AAB59402.1; -  
 DR EMBL; V00544; CAA23805.1; -  
 DR EMBL; V00548; CAA23809.1; -  
 DR EMBL; V00549; CAA23810.1; -  
 DR EMBL; M5486; AAA59181.1; -  
 DR EMBL; M29883; AAA52715.1; -  
 DR EMBL; A04970; CAA00410.1; -  
 DR PIR; A01827; IVH0A2.  
 DR PIR; A01828; IVH0A3.  
 DR PDB; 2HIE; 31-AUG-94.  
 DR PDB; 1RH2; 12-NOV-94.  
 DR PDB; 1ITF; 03-DEC-97.  
 DR GlycoSuiteDB; P01563; -  
 DR MIM; 147562; -  
 DR InterPro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabD; 1.  
 DR PROSITE; PS00252; INTERFERON\_A-B-D; 1.  
 KW Cytokine; Antiviral; Multigene family; Signal; Glycoprotein;  
 KW Polymorphism; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 23  
 FT CHAIN 24 188 INTERFERON ALPHA-2.  
 FT DISULFID 24 121  
 FT DISULFID 52 161  
 FT CARBOHYD 129 129  
 FT VARIANT 46 46  
 FT O-LINKED (GALNAC. . .).  
 FT /FTID-CAR.000049.  
 FT K -> R (IN ALPHA-2B).  
 FT /FTID-VAR.004012.  
 FT SEQUENCE 188 AA; 21550 MW; 101DD21D394CBF97 CRC64;  
 SQ

Query Match 85.7%; Score 36; DB 1; Length 188;  
 Best Local Similarity 87.5%; Pred. No. 3.7;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKISP 8  
 Db 153 LTERKISP 160  
 RESULT 12  
 ID INAT\_HUMAN STANDARD; PRT; 189 AA.  
 AC P01567;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-7 PRECURSOR (INTERFERON ALPHA-J1) (INTERFERON  
 DE ALPHA-J) (LEIF J).  
 GN IFNA7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-86037205; PubMed-4057246;  
 RA Henko K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,  
 RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
 RA Todoroko K., Waelchli M., Nagata S., Weissmann C.;  
 RT "Structural relationship of human interferon alpha genes and  
 RT pseudogenes.";  
 RL J. Mol. Biol. 185:227-260(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83010246; PubMed-6181262;  
 RA Ullrich A., Gray A., Goeddel D.V., Dull J.J.;  
 RT "Nucleotide sequence of a portion of human chromosome 9 containing a  
 RT leukocyte interferon gene cluster.";  
 RL J. Mol. Biol. 156:467-486(1982).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, TEN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 DR EMBL; V00531; CAA23792.1; -  
 DR EMBL; X02960; CAA26706.1; -  
 DR PIR; A01831; IVH0A0.  
 DR HSSP; P01563; 2HIE.  
 DR MIM; 147567; -  
 DR InterPro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabD; 1.  
 DR PROSITE; PS00252; INTERFERON\_A-B-D; 1.  
 KW Cytokine; Antiviral; Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 189 INTERFERON ALPHA-7.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 FT SEQUENCE 189 AA; 22106 MW; 9DF6F5C81E339A42 CRC64;  
 SQ

Query Match 85.7%; Score 36; DB 1; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 3.7;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKXSP 8  
 DB 154 LMEKKXSP 161

RESULT 13  
 INAD\_HUMAN STANDARD: PRT: 189 AA.  
 AC P01570:  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-14 PRECURSOR (INTERFERON ALPHA-H) (LTF H)  
 GN IFNA14.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RP MEDLINE=86037205; PubMed=4057246;  
 RA Henco K., Brosius J., Fujisawa J.-I., Haynes J.R.,  
 RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
 RA Tokokoro K., Waelchli M., Nagata S., Weissmann C.;  
 RT "Structural relationship of human interferon alpha genes and  
 RT pseudogenes";  
 RL J. Mol. Biol. 185:227-260(1985).  
 RP MEDLINE=91201124; PubMed=6165082;  
 RA Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;  
 RT "DNA sequence of two closely linked human leukocyte interferon  
 RT genes";  
 RL Science 212:1159-1162(1981).  
 RP [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81148795; PubMed=6163083;  
 RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,  
 RA McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;  
 RT "The structure of eight distinct cloned human leukocyte interferon  
 RT cDNAs";  
 RL Nature 290:20-26(1981).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYATE SYNTHETASE.  
 CC -1- MISCELLANEOUS: A VARIANT SEQUENCE DIFFERS IN 3 POSITIONS. THE LAST  
 CC 2 BEING THE RESULT OF A DELETION FOLLOWED BY AN INSERTION.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 DR EMBL: V00533; CA23794.1; -  
 DR EMBL: X02959; CA26705.1; -  
 DR EMBL: V00542; CA23803.1; -  
 DR PIR: C23753; IVHU14.  
 DR HSSP: P01563; ZHE.  
 DR MTM: 147579; -  
 DR InterPro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon\_1.  
 DR PRINTS: PR00266; InterferonAB.  
 DR ProDom: PD000550; Interferon\_abd.1.  
 DR SMART: SM00076; Ifabd.1.  
 DR PROSITE: PS00252; INTERFERON\_A\_B\_D.1.  
 DR Cytokine: Antiviral; Multigene family; Glycoprotein; Signal.  
 FT SIGNAL 1 23

FT CHAIN 24 189 INTERFERON ALPHA-14.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISSULFID 52 162 BY SIMILARITY.  
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 175 175 L -> F.  
 FT VARIANT 182 182 /FTID=VAR\_004013.  
 FT VARIANT 184 184 Q -> K.  
 FT VARIANT 184 184 /FTID=VAR\_004015.  
 FT VARIANT 184 184 R -> G.  
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Query Match 85.7%; Score 36; DB 1; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 3.7;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKXSP 8  
 DB 154 LMEKKXSP 161

RESULT 14  
 INA\_FELCA STANDARD: PRT: 194 AA.  
 AC P35849; Q28831;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA PRECURSOR (IFN-ALPHA).  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 NCBI\_TaxID=9685;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92323151; PubMed=1377975;  
 RA Nakamura N., Sudo T., Matsuda S., Yanai A.;  
 RT "Molecular cloning of feline interferon cDNA by direct expression";  
 RL Biosci. Biotechnol. Biochem. 56:211-214(1992).  
 RN [2]  
 RP SEQUENCE OF 1-193 FROM N.A.  
 RX MEDLINE=93291263; PubMed=7685640;  
 RA Ueda Y., Sakurai T., Yanai A.;  
 RT "Homogeneous production of feline interferon in silkworm by replacing  
 RT single amino acid code in signal peptide region in recombinant  
 RT baculovirus and characterization of the product";  
 RL J. Vet. Med. Sci. 55:251-258(1993).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 DR EMBL: S62636; AAB27160.2; -  
 DR PIR: JS0664; JS0664.  
 DR HSSP: P01563; ZHE.  
 DR InterPro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon\_1.  
 DR PRINTS: PR00266; InterferonAB.  
 DR ProDom: PD000550; Interferon\_abd.1.  
 DR SMART: SM00076; Ifabd.1.  
 DR PROSITE: PS00252; INTERFERON\_A\_B\_D.1.  
 DR Cytokine: Antiviral; Multigene family; Glycoprotein; Signal.  
 FT SIGNAL 1 23 BY SIMILARITY.

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FT CHAIN 24 194 INTERFERON ALPHA.
FT DISULFID 24 123 BY SIMILARITY.
FT DISULFID 52 166 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 21 21 S -> V (IN REF. 2).
SQ SEQUENCE 194 AA; 21892 MW; D10E910E3755BFEF CRC64;

Query Match
Best Local Similarity 85.7%; Score 36; DB 1; Length 194;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEEKKYS 8
Db 158 LQKKKYS 165

RESULT 15
IN8_HUMAN STANDARD; PRT; 189 AA.
ID IN8_HUMAN P32881; P09236; P01565;
21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-8 PRECURSOR (INTERFERON ALPHA-B2) (INTERFERON
ALPHA-B) (LEIF B).
GN IFN8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=86037205; PubMed=4057246;
RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
Todoroko K., Melchli M., Nagata S., Weissmann C.;
RT "Structural relationship of human interferon alpha genes and
pseudogenes.";
RL J. Mol. Biol. 185:227-260(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=84183614; PubMed=6325303;
RA Bowden D.W., Mao J., Gill T., Hsiao K., Lillquist J.S., Testa D.,
Vovis G.F.;
RT "Cloning of eukaryotic genes in single-strand phage vectors: the
human interferon genes.";
RL Gene 27:87-99(1984).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=81174733; PubMed=6164048;
RA Yelverton E., Leung D., Meck P., Gray P.W., Goeddel D.V.;
RT "Bacterial synthesis of a novel human leukocyte interferon.";
RL Nucleic Acids Res. 9:731-741(1981).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=81148795; PubMed=6163083;
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte interferon
cDNAs.";
RL Nature 290:20-26(1981).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMS:
A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC -----
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CC -----
DR EMBL: V00545; CAA23806.1; -
DR EMBL: K01900; AAA52716.1; -
DR EMBL: X03125; CAA26903.1; -
DR EMBL: V00550; CAA23811.1; -
DR PIR: D23753; IVH018.
DR PIR: A01829; IVH04.
DR HSSP: P01563; 2HIE.
DR MIM: 147568; -.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR Prodom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabid; 1.
DR PROSITE: PS00252; INTERFERON_A.B.D; 1.
KM Cytokine; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-8.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CONFLICT 8 8 L -> M (IN REF. 3 AND 4).
FT CONFLICT 121 124 SCYW -> VICD (IN REF. 3 AND 4).
SQ SEQUENCE 189 AA; 21989 MW; 83128DA2B6DB2C1 CRC64;

Query Match
Best Local Similarity 83.3%; Score 35; DB 1; Length 189;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEEKKYS 7
Db 154 LQKKKYS 160

RESULT 16
IN01_HORSE STANDARD; PRT; 195 AA.
ID IN01_HORSE AC P05001;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last annotation update)
DE INTERFERON OMEGA-1 PRECURSOR (INTERFERON ALPHA-II-1).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87053170; PubMed=3022999;
RA Himmler A., Hauptmann R., Adolf G.R., Swelly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
I Interferons.";
RL DNA 5:345-356(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=81148795; PubMed=6163083;
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte interferon
cDNAs.";
RL Nature 290:20-26(1981).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMS:
A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M14544; AAA30955.1; -
DR EMBL: A15991; CAA01259.1; -
DR PIR: E24912; IVH021.
DR HSSP: P01563; 1YTF.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.

```

DR Prodom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.  
 FT SIGNAL  
 FT CHAIN 1 23  
 FT DISULFID 24 195 INTERFERON OMEGA-1.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 195 AA: 21882 MW: A81C3CF0A7CA9B6E CRC64;

Query Match 83.3%; Score 35; DB 1; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYS 7  
 Db 154 LTERKYS 160

## RESULT 17

LADL\_MOUSE STANDARD; PRT; 528 AA.  
 AC P57016;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE LADININ 1 (LAD-1) (LINEAR IGA DISEASE AUTOANTIGEN).  
 GN LAD1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Skin;  
 RA MEDLINE=97224461; PubMed=9119369;  
 RX Mochi K., Megahed M., LaForgia S., Uitto J.;  
 RT "Cloning and chromosomal mapping of mouse ladinin, a novel basement  
 membrane zone component.";  
 RL Genomics 39:323-330(1997).

CC -1- FUNCTION: ANCHORING FILAMENT PROTEIN WHICH IS A COMPONENT OF THE  
 CC BASEMENT MEMBRANE ZONE. MAY CONTRIBUTE TO THE STABILITY OF THE  
 CC ASSOCIATION OF THE EPITHELIAL LAYERS WITH THE UNDERLYING  
 CC MESENCHYME. COULD MAINTAIN DERMAL-EPIDERMAL COHESION.  
 CC -1- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX. LOCALIZED TO  
 CC ANCHORING FILAMENTS UNDERLYING HEMIDESMOSES OF THE LAMINA LUCIDA  
 CC OF THE EPIDERMAL BASEMENT MEMBRANE (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY, LUNG AND KERATINOCYTES  
 CC FOLLOWED BY LIVER, SPLEEN AND BRAIN. NOT EXPRESSED IN TESTIS,  
 CC SKELETAL AND HEART MUSCLE AND IN FIBROBLASTS.  
 CC -----  
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 CC -----

DR EMBL; U58011; AAC53044.1; -.  
 DR MGD; MGI:109343; Lad1.  
 KW Extracellular matrix; Basement membrane; Repeat.  
 FT DOMAIN 28 35  
 FT DOMAIN 184 281 6 X SEK REPEATS.  
 FT REPEAT 184 186 SEK 1.  
 FT REPEAT 190 192 SEK 2.  
 FT REPEAT 202 204 SEK 3.  
 FT REPEAT 208 210 SEK 4.  
 FT REPEAT 269 271 SEK 5.  
 FT REPEAT 279 281 SEK 6.  
 SQ SEQUENCE 528 AA: 58863 MW: 3893C72B0C92609C CRC64;

Query Match 81.0%; Score 34; DB 1; Length 528;  
 Best Local Similarity 75.0%; Pred. No. 25;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 Db 219 LTERKYS 226

## RESULT 18

INAA\_HUMAN STANDARD; PRT; 189 AA.  
 AC P01566;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-10 PRECURSOR (INTERFERON ALPHA-C) (LEIF C)  
 DE (INTERFERON ALPHA-6L).  
 GN IFNA10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=81148795; PubMed=6163083;  
 RA Goeddel D.V., Leung D.W., Dull T.O., Gross M., Lawn R.M.,  
 RA McCandless R., Seeburg P.H., Ullrich A., Vetterton E., Gray P.W.;  
 RT "The structure of eight distinct cloned human leukocyte interferon  
 cDNAs.";  
 RL Nature 290:20-26(1981).

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC -----

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 CC -----

DR EMBL; V00551; CAA23812.1; -.  
 DR PIR; A01830; IYHVA5.  
 DR HSSP; P01563; IYF.  
 DR MIM; 147577; -.  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR Prodom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 KW PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Antiviral; Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 189 INTERFERON ALPHA-10.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 SQ SEQUENCE 189 AA: 21835 MW: CEC680996FDA706B CRC64;

Query Match 78.6%; Score 33; DB 1; Length 189;  
 Best Local Similarity 75.0%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 Db 154 LTERKYS 161



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RESULT 19
FVE_FLAVE
ID FVE_FLAVE STANDARD: PRT: 114 AA.
AC P80412;
DR 01-FEB-1995 (Rel. 31, Last sequence update)
DR 01-FEB-1995 (Rel. 31, Last sequence update)
DR 01-NOV-1995 (Rel. 32, Last annotation update)
DE IMMUNOMODULATOR PROTEIN FIP-FVE.
OS Flammulina velutipes.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Tricholomataceae; Flammulina.
OX NCBI_TaxID=38945;
RN [1]
RP MEDLINE=95220348; PubMed=7705335;
RA KO J.-L., Hsu C.-I., Lin R.-H., Kao C.-L., Lin J.-Y.;
RT "A new fungal immunomodulatory protein, FIP-five isolated from the
RT edible mushroom, Flammulina velutipes and its complete amino acid
RT sequence."
RT Eur. J. Biochem. 228:244-249(1995).
-1- SIMILARITY: TO IMMUNOGLOBULIN VARIABLE DOMAINS, BUT LACK THE
CONSERVED DISULFIDE BOND.
KW Acetylation. 1 ACETYLATION (BY SIMILARITY).
FT MOD.RES 114 AA; 12704 MW; D38C64IDCC112A94 CRC64;
SQ SEQUENCE

Query Match 76.2%; Score 32; DB 1; Length 114;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 7
ID 111111
Db 42 LTRKYS 48

RESULT 20
INAL_MOUSE STANDARD: PRT: 189 AA.
AC P01572;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DR 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON ALPHA-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168886; PubMed=6188104;
RX Shaw G.D., Boll W., Taira H., Mantel N., Lengyel P., Weissmann C.;
RT "Structure and expression of cloned murine IFN-alpha genes."
RT Nucleic Acids Res. 11:555-573(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215516; PubMed=2987811;
RX Kelly K.A., Pilha P.M.;
RT "Characterization of a mouse interferon gene locus I. Isolation of a
RT cluster of four alpha interferon genes."
RT Nucleic Acids Res. 13:805-823(1985).
-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
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DR EMBL; X01974; CA26006.1;
DR PIR; A01836; IWSAL.
DR PIR; A23087; A23087.
DR HSP; P01563; 2HIE.
DR MGD; MGI:107668; Ifnal.
DR InterPro; IP000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Cytokine; Glycoprotein; Antiviral; Multigene family; signal.
KW SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-1.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (PROBABLE).
SQ SEQUENCE 189 AA; 21634 MW; 553B4679A4D310BE CRC64;

Query Match 73.8%; Score 31; DB 1; Length 189;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKYS 8
ID 111111
Db 154 LTRKNSP 161

RESULT 21
INAL_PIG STANDARD: PRT: 189 AA.
AC P49879;
DR 01-OCT-1996 (Rel. 34, Created)
DR 01-OCT-1996 (Rel. 34, Last sequence update)
DR 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERFERON ALPHA-1 PRECURSOR (IFN-ALPHA-1).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DOMESTICA; TISSUE=Liver;
RX MEDLINE=92193689; PubMed=1800582;
RX Lefevre F., la Bonnardiere C., Mege D.;
RT "The porcine family of interferon-omega: cloning, structural
RT analysis, and functional studies of five related genes."
RT J. Interferon Res. 11:341-350(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87035119; PubMed=2945869;
RX Lefevre F., la Bonnardiere C.;
RT "Molecular cloning and sequencing of a gene encoding biologically
RT active porcine alpha-interferon."
RT J. Interferon Res. 6:349-360(1986).
-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
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CC -----
DR EMBL: X57191; CAA40477.1; -
DR EMBL: M28623; AAA31053.1; -
DR HSSP: P01563; 1TFE
DR InterPro: IPR000477.1; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 1 23
FT DISULFID 24 189
FT DISULFID 24 122
FT DISULFID 52 162
FT DISULFID 101 162
SQ SEQUENCE 189 AA; 21433 MW; 8C8BEA8DEAAE3334 CRC64;

```

```

Query Match
Best Local Similarity 73.8%; Score 31; DB 1; Length 189;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 LTERKXSP 8
Db 154 LQEKXSP 161

```

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RESULT 22
IN6_MOUSE STANDARD; PRT; 189 AA.
ID IN6_MOUSE
AC P07350;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON ALPHA-5 PRECURSOR.
GN IFNA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8521516; PubMed=2987811;
RA Kelly K.A., Pitba P.M.;
RT "Characterization of a mouse interferon gene locus I. Isolation of a
RT cluster of four alpha interferon genes."
RL Nucleic Acids Res. 13:805-823(1985).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
DR EMBL: X01971; CAA26003.1; ALT_SEQ.
DR PIR: C23087; IVMSA5.
DR HSSP: P01563; 2HIE.
DR MGD: MGI:107663; Ifna5.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 23

```

```

FT CHAIN 24 189
FT DISULFID 24 122
FT DISULFID 52 162
FT CARBOHYD 101 101
SQ SEQUENCE 189 AA; 21514 MW; 8BB9CDFD15FC3BD CRC64;

```

```

Query Match
Best Local Similarity 73.8%; Score 31; DB 1; Length 189;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LTERKXSP 8
Db 154 LQEKXSP 161

```

```

RESULT 23
IN6_MOUSE STANDARD; PRT; 189 AA.
ID IN6_MOUSE
AC P07350;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON ALPHA-6 PRECURSOR.
GN IFNA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C;
RA MEDLINE=8521516; PubMed=2987811;
RA Kelly K.A., Pitba P.M.;
RT "Characterization of a mouse interferon gene locus I. Isolation of a
RT cluster of four alpha interferon genes."
RL Nucleic Acids Res. 13:805-823(1985).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
DR EMBL: X01972; CAA26004.1; -
DR PIR: D23087; IVMSA6.
DR HSSP: P01563; 2HIE.
DR MGD: MGI:107662; Ifna6.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Signal; Antiviral; Multigene family; Glycoprotein.
FT SIGNAL 1 23
FT CHAIN 24 189
FT DISULFID 24 122
FT DISULFID 52 162
FT CARBOHYD 101 101
SQ SEQUENCE 189 AA; 21499 MW; A960BC251330684 CRC64;

```

```

Query Match
Best Local Similarity 73.8%; Score 31; DB 1; Length 189;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 LREKXSP 8  
| | | | |  
Db 154 LREKXSP 161

## RESULT 24

INAB\_MOUSE STANDARD: PRT: 189 AA.  
ID INAB\_MOUSE  
AC P17660;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE INTERFERON ALPHA-8 PRECURSOR.  
GN IFNA8 OR IFA8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89279315; PubMed=2471809;  
RA Navarro S., Dion M., Vlodavsky G., Berlot-Picard F., Doly J.;  
RT "Isolation and characterization of a functional murine Interferon  
alpha gene which is not expressed in fibroblasts upon virus  
induction.";  
RT J. Gen. Virol. 70:1381-1389(1989).  
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
CC -1- MISCELLANEOUS: MURINE INTERFERON ALPHA-8 IS NOT EXPRESSED IN  
CC FIBROBLASTS UPON VIRUS INDUCTION.  
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.

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CC -----

DR EMBL: D00460; BAA00349.1; -.  
DR HSSP: P01563; 2HIE.  
DR MGD: MGI:107660; Ifna8.  
DR InterPro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon\_1.  
DR PRINTS: PR000266; InterferonAB.  
DR ProDom: PD000550; Interferon\_abd; 1.  
DR SMART: SM00076; IFab; 1.  
DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.  
KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.  
FT CHAIN 1 189  
FT SIGNAL 24 23  
FT CHAIN 24 189  
FT DISULFID 24 122  
FT DISULFID 52 162  
FT CARBOHYD 101 101  
SQ SEQUENCE 189 AA; 21469 MW; 0960AD342C98EB32 CRC64;

Query Match 73.8%; Score 31; DB 1; Length 189;  
Best Local Similarity 75.0%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LREKXSP 8  
| | | | |  
Db 154 LREKXSP 161

RESULT 25  
INAB\_MOUSE STANDARD: PRT: 190 AA.  
ID INAB\_MOUSE

AC P01573;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE INTERFERON ALPHA-2 PRECURSOR.  
GN IFNA2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83168886; PubMed=6188104;  
RA Shaw G.D., Boll W., Taira H., Maneti N., Lengyel P., Weissmann C.;  
RT "Structure and expression of cloned murine IFN-alpha genes.";  
RT Nucleic Acids Res. 11:555-573(1983).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85215515; PubMed=2987810;  
RA Zwartthoff E.C., Mooren A.T.A., Trapman J.;  
RT "Organization, structure and expression of murine interferon alpha  
genes.";  
RT Nucleic Acids Res. 13:791-804(1985).

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CC -----

DR EMBL: K01238; AAA37887.1; -.  
DR EMBL: X01969; AAA26002.1; -.  
DR PIR: A01837; IVMSA2.  
DR HSSP: P01563; 2HIE.  
DR MGD: MGI:107666; Ifna2.  
DR InterPro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon\_1.  
DR PRINTS: PR000266; INTERFERONAB.  
DR ProDom: PD000550; Interferon\_abd; 1.  
DR SMART: SM00076; IFab; 1.  
DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.  
KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.  
FT CHAIN 1 190  
FT SIGNAL 24 23  
FT CHAIN 24 190  
FT DISULFID 24 122  
FT DISULFID 52 162  
FT CARBOHYD 101 101  
SQ SEQUENCE 190 AA; 21921 MW; EFA97FC69C300FD5 CRC64;

Query Match 73.8%; Score 31; DB 1; Length 190;  
Best Local Similarity 75.0%; Pred. No. 36;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Search completed: January 15, 2002, 08:44:51  
Job time: 287 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:36:43 ; Search time 22.55 Seconds  
(without alignments)  
27.024 Million cell updates/sec

Title: US-09-424-080a-1

Perfect score: 42  
Sequence: 1 LFEKKYSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 50 summaries

Database :  
1: PIR\_68:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	72	2 I79343	interferon alpha-T
2	42	100.0	167	2 E25843	interferon alpha-F
3	42	100.0	167	2 D25843	interferon alpha-G
4	42	100.0	176	2 I56314	interferon alpha-H
5	42	100.0	181	2 I56313	interferon alpha-I
6	42	100.0	189	1 IVH016	interferon alpha-I
7	42	100.0	189	1 IVH017	interferon alpha-I
8	42	100.0	189	1 IVH018	interferon alpha-I
9	42	100.0	189	1 IVH019	interferon alpha-I
10	42	100.0	189	1 IVH020	interferon alpha-I
11	42	100.0	189	1 IVH021	interferon alpha-I
12	42	100.0	189	2 I52347	interferon alpha-M
13	42	100.0	189	2 I84464	interferon alpha-F
14	42	100.0	189	2 I53102	interferon alpha-F
15	42	100.0	189	2 I51970	interferon precurs
16	36	85.7	165	2 I78570	interferon
17	36	85.7	167	2 F25843	interferon alpha-J
18	36	85.7	170	2 A48772	interferon, atypic
19	36	85.7	184	1 IVH044	interferon alpha-I
20	36	85.7	184	1 IVH042	interferon alpha-I
21	36	85.7	184	1 IVH043	interferon alpha-I
22	36	85.7	184	1 IVH041	interferon alpha-I
23	36	85.7	188	1 IVH042	interferon alpha-2
24	36	85.7	189	1 IVH014	interferon alpha-1
25	36	85.7	189	1 IVH040	interferon alpha-7
26	36	85.7	194	2 JS0664	interferon precurs
27	36	85.7	730	2 H86295	hypothetical prote
28	35	83.3	162	2 C25843	interferon alpha-B
29	35	83.3	189	1 IVH044	interferon alpha-4

30	35	83.3	189	1 IVH018	interferon alpha-I
31	35	83.3	189	1 IVH021	interferon alpha-I
32	33	78.6	110	2 F85431	hypothetical prote
33	33	78.6	189	1 IVH045	interferon alpha-5
34	33	78.6	221	2 D86051	hypothetical prote
35	32	76.2	114	2 S69147	immunomodulatory p
36	32	76.2	414	2 D96524	protein TIM15.3 f1
37	32	76.2	573	2 T27578	hypothetical prote
38	32	76.2	1528	2 T37308	ATPase homolog - C
39	31	73.8	189	1 IVMSA5	interferon alpha-1
40	31	73.8	189	1 IVMSA1	interferon alpha-1
41	31	73.8	189	1 IVMSA6	interferon alpha-1
42	31	73.8	189	2 S23709	interferon alpha-1
43	31	73.8	189	2 I49773	murine interferon
44	31	73.8	190	2 IVMSA2	interferon alpha-2
45	31	73.8	190	2 JH0468	interferon alpha-1
46	31	73.8	190	2 A24401	interferon alpha-1
47	31	73.8	190	2 I49772	interferon alpha-7
48	31	73.8	190	2 I49775	interferon alpha-B
49	31	73.8	190	2 I49774	interferon -
50	31	73.8	197	2 A70033	carbonic anhydrase

## ALIGNMENTS

RESULT 1  
I79343  
Interferon alpha-T - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 16-Jul-1999  
C:Accession: I79343  
R:lund, B.; Edlund, T.; Lindemaier, W.; Ny, T.; Collins, J.; Lundgren, E.; von Gabai  
Proc. Natl. Acad. Sci. U.S.A. 81, 2435-2439, 1984  
A:Title: Novel cluster of alpha-interferon gene sequences in a placental cosmid DNA 1  
A:Reference number: 158999; MUID:84194022  
A:Accession: I79343  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-72 <RES>  
A:Cross-references: GB:K01461; NID:g184575; PIDN:AAA58685.1; PID:g184579  
C:Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFEKKYSP 8  
DB 65 LFEKKYSP 72

## RESULT 2

E25843  
Interferon alpha-F - human  
N:Alternate names: human leukocyte interferon (IFN)  
C:Species: Homo sapiens (man)  
C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 15-Jun-1996  
C:Accession: E25843  
R:Ohara, O.; Teraoka, H.  
FEBS Lett. 211, 78-82, 1987  
A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide  
A:Reference number: A91374; MUID:87105954  
A:Accession: E25843  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-167 <OH>  
C:Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTERKYSK 8  
 |||||  
 Db 132 LTERKYSK 139

RESULT 3  
 D25843  
 Interferon alpha-G - human  
 N:Alternate names: human leukocyte interferon (IFN)  
 C:Species: Homo sapiens (man)  
 C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 15-Jun-1996  
 C:Accession: D25843  
 R:Ohara, O.; Teraoka, H.  
 FEBS Lett. 211, 78-82, 1987  
 A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel  
 A:Reference number: A91374; MUID:87105934  
 A:Accession: D25843  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-167 <OHA>  
 C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
 |||||  
 Db 132 LTERKYSK 139

RESULT 4  
 I56314  
 Interferon-alpha - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I56314  
 R:Lund, B.; von Gabain, A.; Edlund, T.; Ny, T.; Lundgren, E.  
 J. Interferon Res. 5, 229-238, 1985  
 A:Title: Differential expression of interferon genes in a substrain of Namalva cells.  
 A:Reference number: I56314; MUID:85235859  
 A:Accession: I56314  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-176 <RES>  
 A:Cross-references: GB:M71246; NID:g184572; PIDN:AAA52713.1; PID:g184573  
 C:Genetics:  
 A:Gene: IFNA  
 C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 0.26;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
 |||||  
 Db 141 LTERKYSK 148

RESULT 5  
 I56313  
 Interferon alpha 21 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I56313  
 R:Geren, E.; Beizin, V.M.; Jansone, I.; Tsimanis, A.; Vishnevsky, Y.; Apsalons, U.  
 J. Interferon Res. 4, 609-617, 1984  
 A:Title: Novel human leukocyte interferon subtype and structural comparison of alpha int  
 A:Reference number: I56313; MUID:85056523

A:Accession: I56313  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-181 <RES>  
 A:Cross-references: GB:M28586; NID:g184636; PIDN:AAA36041.1; PID:g306912  
 C:Genetics:  
 A:Gene: GDB:IFNA21  
 A:Cross-references: GDB:136360; OMIM:147584  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 0.27;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
 |||||  
 Db 146 LTERKYSK 153

RESULT 6  
 I1VH016  
 Interferon alpha-I-6 precursor - human  
 N:Alternate names: HuIFN-alpha-I-6; LeIF K; type I interferon  
 C:Species: Homo sapiens (man)  
 C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: A23753  
 R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: A23753  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: GB:X02958; NID:g32662; PIDN:CAA26704.1; PID:g758080  
 C:Genetics:  
 A:Gene: GDB:IFNA6  
 A:Cross-references: GDB:136363; OMIM:147566  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: interferon alpha-I-6 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
 |||||  
 Db 154 LTERKYSK 161

RESULT 7  
 I1VH017  
 Interferon alpha-5 precursor - human  
 N:Alternate names: Interferon alpha-G  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Sep-1981 #sequence\_revision 29-Jan-1999 #text\_change 21-Jul-2000  
 C:Accession: S43716; A01833  
 R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: S43716  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: EMBL:X02956; NID:g32659; PIDN:CAA26702.1; PID:g758079  
 R:Coeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb  
 Nature 290, 20-26, 1981

A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: A01833  
 A:Molecule type: mRNA  
 A:Residues: 57-189 <GOE>  
 A:Cross-references: GB:V00541; GB:J00213; NID:932718; PIDN:CAA23802.1; PID:932719  
 A>Note: eight classes of interferon alpha clones were identified; this sequence is derived from C:Genetics:  
 A:Gene: GDB:IFNA5  
 A:Cross-references: GDB:136362; OMIM:147565  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-5 #status predicted <MAT>

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
 |||||||  
 Db 154 LTERKXSP 161

## RESULT 8

IVH041  
 N:Alternate names: Interferon alpha-13; Interferon alpha-D; Interferon alpha-I-1  
 C:Species: Homo sapiens (man)  
 C:Date: 22-May-1981 #sequence\_revision 01-Sep-1981 #text\_change 24-Sep-1999  
 C:Accession: C23285; A91467; A93249; I58213; S43715; S41196; A01826  
 R:Gordon, D.J.; Shepard, H.M.; Goeddel, D.V.  
 M01.Cell: Biol. 5, 768-779, 1985  
 A:Title: Two distinct families of human and bovine interferon-alpha genes are coordinate  
 A:Reference number: A93070; MUID:85187974  
 A:Accession: C23285  
 A:Molecule type: DNA  
 A:Residues: 1-189 <CAP>  
 R:Mantel, N.; Schwartzstein, M.; Streuli, M.; Panem, S.; Nagata, S.; Weissmann, C.  
 Gene 10, 1-10, 1980  
 A:Title: The nucleotide sequence of a cloned human leukocyte interferon cDNA.  
 A:Reference number: A91467; MUID:8105094  
 A:Accession: A91467  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <MAN>  
 A:Cross-references: GB:V00537; NID:932711; PIDN:CAA23798.1; PID:932712  
 R:Taniguchi, T.; Mantel, N.; Schwartzstein, M.; Nagata, S.; Muramatsu, M.; Weissmann, C.  
 Nature 285, 547-549, 1980  
 A:Title: Human leukocyte and fibroblast interferons are structurally related.  
 A:Reference number: A93226; MUID:80254543  
 A:Accession: A93226  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <MAN>  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: A93249  
 A:Molecule type: mRNA  
 A:Residues: 1-136, 'V', 138-189 <GOE>  
 A:Cross-references: GB:V00538; NID:932713; PIDN:CAA23799.1; PID:932714  
 A>Note: eight classes of interferon alpha clones were identified; this sequence is derived from C:Genetics:  
 A:Gene: GDB:IFNA5  
 A:Cross-references: GDB:136362; OMIM:147565  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-5 #status predicted <MAT>

R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: S43715  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: EMBL:X75934  
 R:Roostoks, N.  
 Submitted to the EMBL Data Library, December 1993  
 A:Reference number: S41196  
 A:Accession: S41196  
 A:Molecule type: DNA  
 A:Residues: 1-9, 'A', 11-189 <ROS>  
 A:Cross-references: EMBL:X75934; NID:9439666; PIDN:CAA53538.1; PID:9439667  
 C:Genetics:  
 A:Gene: GDB:IFNA1  
 A:Cross-references: GDB:136353; OMIM:147660  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-1 #status predicted <MAT>  
 F:24-122, 52-162/Disulfide bonds: #status predicted

## Query Match

100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
 |||||||  
 Db 154 LTERKXSP 161

## RESULT 9

IVH04  
 N:Alternate names: Interferon alpha-I-F precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 28-May-1999  
 C:Accession: A01832  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: A01832  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <GOE>  
 A:Cross-references: GB:V00540; GB:J00212; NID:932716; PIDN:CAA23801.1; PID:932717  
 A>Note: eight classes of interferon alpha clones were identified; this sequence is derived from C:Genetics:  
 A:Gene: GDB:IFNA1  
 A:Cross-references: GDB:119328; OMIM:147660  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-I-F #status predicted <MAT>  
 F:24-122, 52-162/Disulfide bonds: #status predicted

## Query Match

100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
 |||||||  
 Db 154 LTERKXSP 161

## RESULT 10

IVH04B

interferon alpha-I-4b precursor - human  
N:Alternate names: HuIFN-alpha-I-4b; type I interferon  
C:Species: Homo sapiens (man)  
C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
C:Accession: E23753  
R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov  
J. Mol. Biol. 185, 227-260, 1985  
A>Title: Structural relationship of human interferon alpha genes and pseudogenes.  
A:Reference number: A92916; MUID:86037205  
A:Accession: E23753  
A:Molecule type: DNA  
A:Residues: 1-189 <RES>  
A:Cross-references: GB:X02955; NID:g32656; PIDN:CAA26701.1; PID:g758078  
C:Genetics:  
A:Gene: GDB:IFNA1  
A:Cross-references: GDB:119328; OMIM:147660  
A:Map position: 9p22-9p22  
C:Superfamily: Interferon alpha  
C:Keywords: antiviral  
A>Title: 23/Domain: signal sequence #status predicted <SIG>  
F:24-189/Product: interferon alpha-I-4b #status predicted <MAT>  
F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKXSP 8  
DB 154 LTERKXSP 161

RESULT 11  
IYHUA9  
interferon alpha-17 precursor - human  
N:Alternate names: Interferon alpha-9; interferon alpha-I'  
C:Species: Homo sapiens (man)  
C>Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jul-2000  
C:Accession: A01835; A22255; C42753  
R:Law, R.M.; Adelstein, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.  
Science 212, 1159-1162, 1981  
A>Title: DNA sequence of two closely linked human leukocyte interferon genes.  
A:Reference number: A94255; MUID:81201124  
A:Accession: A01835  
A:Molecule type: DNA  
A:Residues: 1-189 <LAM>  
A:Cross-references: GB:J00216; GB:V00532; NID:g32633; PIDN:CAA23793.1; PID:g32634  
R:Mizoguchi, J.; Pitha, P.M.; Raj, N.B.K.  
DNA 4, 221-232, 1985  
A>Title: Efficient expression in Escherichia coli of two species of human interferon- $\alpha$   
A:Reference number: A22255; MUID:85229953  
A:Accession: A22255  
A:Molecule type: mRNA  
A:Residues: 1-56, 'H', 58-189 <MI2>  
A:Cross-references: GB:M1026; NID:g184612; PIDN:AA52725.1; PID:g306908  
R:Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,  
J. Biol. Chem. 267, 15210-15216, 1992  
A>Title: Purification and characterization of multiple components of human lymphoblastoid  
A:Reference number: A42753; MUID:92340576  
A:Accession: C42753  
A:Molecule type: protein  
A:Residues: 'X', 25-50, 'XX', 53-56 <ZOO>  
C:Genetics:  
A:Gene: GDB:IFNA17  
A:Cross-references: GDB:136358; OMIM:147583  
A:Map position: 9p22-9p22  
C:Superfamily: Interferon alpha  
C:Keywords: leukocyte  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-189/Product: interferon alpha-17 #status predicted <MAT>  
F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 154 LTERKXSP 161

RESULT 12  
I52347  
interferon alpha-M1 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I52347  
R:Linane, A.W.; Bellharz, M.W.; McMullen, G.L.; Macreadie, I.G.; Murphy, M.; Nisbet,  
Biochem. Int. 8, 725-732, 1984  
A>Title: Nucleotide sequence and expression in E. coli of a human interferon-alpha ge  
A:Reference number: I52347; MUID:84307815  
A:Accession: I52347  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-189 <RES>  
A:Cross-references: GB:M27318; NID:g184617; PIDN:AA52726.1; PID:g306909  
C:Genetics:  
A:Gene: IFNA  
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 154 LTERKXSP 161

RESULT 13  
I84464  
interferon-alpha-F - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
C:Accession: I84464; I37583  
R:Gren, E.Y.; Betzlin, V.M.; Tsimanis, A.Y.; Apsalon, U.R.; Vishnevskii, Y.I.; Yansone  
A.; Lozha, V.P.; Kavan, V.M.; Efimov, V.A.; Sverdlov, E.D.  
Dokl. Biochem. 269, 91-95, 1983  
A>Title: A new type of leukocytic interferon.  
A:Reference number: I37583  
A:Accession: I84464  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-189 <RES>  
A:Cross-references: GB:M12350; NID:g184598; PIDN:AA52718.1; PID:g306906  
A:Accession: I37583  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-189 <RES>  
A:Cross-references: EMBL:X00145; NID:g32724; PIDN:CAA24980.1; PID:g32725  
C:Genetics:  
A:Gene: IFNA  
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 154 LTERKXSP 161



## RESULT 14

I53102

Interferon-alpha-J1 - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I53102

R:Cohen, S.; Veljan, B.; Grosfeld, H.; Shalita, Z.; Leitner, M.; Shaffer, A.

Dev. Biol. Stand. 60, 111-122, 1985

A:Title: Cloning, expression and biological activity of a new variant of human interferon

A:Reference number: I53102; MUID:86005847

A:Accession: I53102

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-189 &lt;RES&gt;

A:Cross-references: GB:M34913; NID:q184614; PIDN:AAA36039.1; PID:q184615

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 100.0%; Score 42; DB 2; Length 189;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 154 LTRKXSP 161

## RESULT 15

I51970

Interferon precursor - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I51970

R:Cavelier, V.I.; Zlochevsky, M.L.; Sorokin, A.V.; Natoditskaya, V.A.; Bolotin, A.P.; De

Antibiot. Med. Biotechnol. 31, 352-356, 1986

A:Title: Cloning and the determination of the nucleotide sequences in 2 genes of human

A:Reference number: I51970; MUID:87024453

A:Accession: I51970

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-189 &lt;RES&gt;

A:Cross-references: GB:M38289; NID:q186407; PIDN:AAA59165.1; PID:q186408

C:Genetics:

A:Gene: IFNA

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 100.0%; Score 42; DB 2; Length 189;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 154 LTRKXSP 161

## RESULT 16

I78570

Alpha 2 Interferon - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999

C:Accession: I78570

R:Weber, H.; Weismann, C.

Nucleic Acids Res. 11, 5661-5669, 1983

A:Title: Formation of genes coding for hybrid proteins by recombination between related

A:Reference number: I58213; MUID:8329241

A:Accession: I78570

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-165 &lt;RES&gt;

A:Cross-references: GB:M29883; NID:q184585; PIDN:AAA52715.1; PID:q386795

C:Genetics:

A:Gene: IFNA  
C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 85.7%; Score 36; DB 2; Length 165;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 130 LTRKXSP 137

## RESULT 17

F25843

Interferon alpha-J - human

N:Alternate names: human leukocyte interferon (IFN)

C:Species: Homo sapiens (man)

C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 15-Jun-1996

C:Accession: F25843

R:Ohara, O.; Terakura, H.

FEBS Lett. 211, 78-82, 1987

A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide

A:Reference number: A91374; MUID:87105954

A:Accession: F25843

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-167 &lt;OHA&gt;

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 85.7%; Score 36; DB 2; Length 167;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 132 LTRKXSP 139

## RESULT 18

A48772

Interferon, atypical type I precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 24-Nov-1999

C:Accession: A48772

R:DeFeve, F.; Boulay, V.

J. Biol. Chem. 268, 19760-19768, 1993

A:Title: A novel and atypical type one interferon gene expressed by trophoblast durin

A:Reference number: A48772; MUID:93374975

A:Accession: A48772

A:Status: preliminary

A:Molecule type: DNA; mRNA

A:Residues: 1-170 &lt;LEF&gt;

A:Cross-references: GB:22706; NID:q414202; PIDN:CAA80407.1; PID:q414203

C:Genetics:

A:Introns: #status absent

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 85.7%; Score 36; DB 2; Length 170;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 146 LTRKXSP 153

## RESULT 19

IVH0A4

Interferon alpha-I-4 precursor - horse

N:Alternate names: EqIFN-alpha-I-4; type I interferon

C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: D24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: D24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4543; NID:9164224; PIDN:AAA30952.1; PID:9164225  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-4 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 20

IVHOA2  
 Interferon alpha-I-2 precursor - horse  
 N:Alternate names: EqIFN-alpha-I-2; type I interferon  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: B24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: B24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4541; NID:9164218; PIDN:AAA30950.1; PID:9164221  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-2 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 21

IVHOA3  
 Interferon alpha-I-3 precursor - horse  
 N:Alternate names: EqIFN-alpha-I-3; type I interferon  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: C24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: C24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4542; NID:9164222; PIDN:AAA30951.1; PID:9164223

C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-3 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 22

IVHOA1  
 Interferon alpha-I-1 precursor - horse  
 N:Alternate names: EqIFN-alpha-I-1; type I interferon  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: A24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: A24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4540; NID:9164226; PIDN:AAA30953.1; PID:9164227  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-1 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 23

IVHOA2  
 Interferon alpha-2 precursor (allele a) [validated] - human  
 N:Alternate names: IFN-alpha2; interferon alpha-3; interferon alpha-A; leukocyte interferon  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Oct-1980 #sequence\_revision 01-Sep-1991 #text\_change 08-Dec-2000  
 C:Accession: A93234; D93249; A93888; A94252; A25843; A01828; C61478; S15848;  
 R:Goeddel, D.V.; Yelverton, E.; Ullrich, A.; Heyneker, H.L.; Moczart, G.; Holmes, W.  
 ss, M.; Familletti, P.C.; Pestka, S.  
 Nature 287, 411-416, 1980  
 A:Title: Human leukocyte interferon produced by Escherichia coli is biologically active  
 A:Reference number: A93234; MUID:81052322  
 A:Accession: A93234  
 A:Molecule type: DNA  
 A:Residues: 1-188 <GO>  
 A:Cross-references: GB:V00544; NID:932730; PIDN:CAA23805.1; PID:932731  
 A:Experimental source: Clone pL31  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: D93249  
 A:Molecule type: mRNA  
 A:Residues: 1-188 <GO>  
 A:Cross-references: GB:V00549; NID:932744; PIDN:CAA23810.1; PID:932745  
 A>Note: eight classes of interferon alpha clones were identified; this sequence is de

R:Lawn, R.M.; Gross, M.; Houck, C.M.; Franke, A.E.; Gray, P.V.; Goeddel, D.V.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 5435-5439, 1981  
 A:Title: DNA sequence of a major human leukocyte interferon gene.  
 A:Reference number: A93888; MUID:82060261  
 A:Accession: A93888  
 A:Molecule type: DNA  
 A:Residues: 1-45, 'R', 47-188 <LAN>  
 A:Cross-references: GB:J00207; NID:q184581; PIDN:AA59402.1; PID:q386793  
 A:Experimental source: clone lambda-alpha-2  
 R:Oliver, G.; Balbas, P.; Valle, F.; Soberon, X.; Bolivar, F.  
 Rev. Latinoam. Microbiol. 27, 141-150, 1985  
 A:Title: Cloning of human leukocyte interferon cDNA and a strategy for its production  
 A:Reference number: I59458; MUID:86069501  
 A:Accession: I59458  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-188 <RES>  
 A:Cross-references: GB:M54886; NID:q186498; PIDN:AA59181.1; PID:q186499  
 R:Streuli, M.; Nagata, S.; Weissmann, C.  
 Science 209, 1343-1347, 1980  
 A:Title: At least three human type alpha interferons: structure of alpha2.  
 A:Reference number: A94252; MUID:81015442  
 A:Accession: A94252  
 A:Molecule type: mRNA  
 A:Residues: 7-45, 'R', 47-188 <STR>  
 A:Cross-references: GB:V00348; NID:q32740; PIDN:CAA33809.1; PID:q32741  
 R:Ohara, O.; Teraoka, H.  
 FEBS Lett. 211, 78-82, 1987  
 A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel  
 A:Reference number: A91374; MUID:87105954  
 A:Accession: A25843  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 'M', 24-188 <CHA>  
 A:Note: engineered sequence of mature form expressed in *Escherichia coli*  
 R:Allen, G.; Fantes, K.H.  
 Nature 287, 408-411, 1980  
 A:Title: A family of structural genes for human lymphoblastoid (leukocyte-type) interferon  
 A:Reference number: A01828; MUID:81052321  
 A:Accession: A01828  
 A:Molecule type: protein  
 A:Residues: 24-42, 'Z', 44-45, 'R', 47-74, 'A', 76, 'S', 78-98, 'X', 100-105, 'D', 107-109, 'P', 111-113  
 A:Note: residues at positions 83, 86, and 139 may be Ile or possibly Leu; those at position 57-Arg, 75-Thr, 77-Pro, and 96-Glx were also found  
 R:Fukuda, S.; Ando, S.; Sanou, O.; Tanaka, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Arimura, H.  
 Lymphokine Res. 7, 175-185, 1988  
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and -gamma  
 A:Reference number: A61478; MUID:88301617  
 A:Accession: C61478  
 A:Molecule type: protein  
 A:Residues: 24-45, 'R', 47-53 <FKK>  
 A:Experimental source: B-cell lymphoblastoid cell line BALL-1  
 R:Adolf, G.R.; Kalsner, I.; Ahorn, H.; Maurer-Fogy, I.; Cantell, K.  
 Biochem. J. 276, 511-518, 1991  
 A:Title: Natural human interferon-alpha-2 is O-glycosylated.  
 A:Reference number: S15848; MUID:91264809  
 A:Accession: S15848  
 A:Molecule type: protein  
 A:Residues: 24-45, 'R', 47-53 <BIO>  
 A:Experimental source: leukocytes  
 R:Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu, J.; Biol. Chem. 267, 15210-15216, 1992  
 A:Title: Purification and characterization of multiple components of human lymphoblastoid interferon  
 A:Reference number: A42753; MUID:92340576  
 A:Accession: B42753  
 A:Molecule type: protein  
 A:Residues: 'X', 25-45, 'R', 47-51, 'X', 53-55, 'XX', 58-65 <ZOO>  
 A:Experimental source: Sendai virus-induced Namalwa cells  
 R:Metzel, R.  
 Nature 289, 606-607, 1981  
 A:Title: Assignment of the disulphide bonds of leukocyte interferon.  
 A:Reference number: A93244; MUID:81123083  
 A:Contents: annotation; disulfide bonds

R:Murgolo, N.J.; Windsor, W.T.; Hruza, A.; Reichert, P.; Tsaropoulos, A.; Baldwin, S  
 Proteins 17, 62-74, 1993  
 A:Title: A homology model of human interferon alpha-2.  
 A:Reference number: A44748; MUID:94052087  
 A:Contents: annotation; theoretical model  
 R:Gewert, D.; Salom, C.; Barber, K.; Macbride, S.; Cooper, H.; Lewis, A.; Weed, J.; C  
 J. Interferon Res. 13, 227-231, 1993  
 A:Title: Analysis of interferon-alpha 2 sequences in human genomic DNA.  
 A:Reference number: I56312; MUID:93375201  
 A:Accession: I56312  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-72 <REM>  
 A:Cross-references: GB:S64979; NID:q408874; PIDN:AA013960.1; PID:q4261660  
 R:Zhao, X.X.; Li, B.L.; Langer, J.A.; Van Riper, G.; Pestka, S.  
 Anal. Biochem. 178, 342-347, 1989  
 A:Title: Construction and phosphorylation of a fusion protein Hu-IFN-alpha A/gamma.  
 A:Reference number: I36908; MUID:89321045  
 A:Accession: I36909  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'M', 24-188 <RE2>  
 A:Cross-references: EMBL:X15631; NID:q22771; PIDN:CAA33638.1; PID:q22772  
 C:Genetics:  
 A:Gene: GDB:IFNA2  
 A:Cross-references: GDB:I36359; OMIM:147562  
 A:Map position: 9p22-9p22  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral; cytokine; glycoprotein; leukocyte  
 F1-23/Domain: signal sequence #status predicted <SIG>  
 F124-188/Prodomain: interferon alpha-2 #status experimental <MAT>  
 F124-121,52-161/Disulfide bonds: #status experimental  
 F129/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 85.7% Score 36; DB 1; Length 188;  
 Best Local Similarity 87.5% Pred. No. 4.9;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKEKKYSP 8  
 DB 153 LKEKKYSP 160

RESULT 24  
 IYH014  
 Interferon alpha-I-14 precursor [validated] - human  
 M:Alternate names: HuIFN-alpha-I-14; lambda-2-h: type I interferon  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Sep-1981 #sequence-revision 01-Sep-1981 #text-change 08-Dec-2000  
 C:Accession: A92916; A94255; B93249; PC2203; A01834; C23753  
 R:Holm, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: A92916  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: GB:X02959; NID:q32650; PIDN:CAA26705.1; PID:q758076  
 R:Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.  
 Science 212, 1159-1162, 1981  
 A:Title: DNA sequence of two closely linked human leukocyte interferon genes.  
 A:Reference number: A94255; MUID:81201124  
 A:Accession: A94255  
 A:Molecule type: DNA  
 A:Residues: 1-189 <LAM>  
 A:Cross-references: GB:V00533; GB:J00215; NID:q32635; PIDN:CAA23794.1; PID:q32636  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: B93249  
 A:Molecule type: mRNA

A:Residues: 1-174, 'F', 176-189 <GOE>  
 A:Cross-references: GB:V00542; GB:J00214; NID:q32720; PIDN:CAA23803.1; PID:q32721  
 A:Note: a variant sequence differs from that shown in having 175-Phe, 182-Lys, and 184-C  
 R:Shiono, H.; Koga, J.; Uemura, H.; Matsuo, A.  
 Biosci. Biotechnol. Biochem. 58, 1714-1715, 1994  
 A:Title: Identification of glycosylated subtypes of interferon-alpha produced by human 1  
 A:Reference number: PC2203; MUID:55036878  
 A:Accession: PC2203  
 A:Molecule type: Protein  
 A:Residues: 'X', 25-43 <SHI>  
 A:Experimental source: Leukocyte  
 C:Genetics:  
 A:Gene: GDB:IFNA14  
 A:Cross-references: GDB:136356; OMIM:147579  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; glycoprotein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-I-14 #status experimental <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted  
 F:25,95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.7% Score 36; DB 1; Length 189;  
 Best Local Similarity 87.5% Pred. No. 4.9;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LTERKYP 8  
 I I I I I I I I  
 Db 154 LMEKKYSP 161

## RESULT 25

IVH0A0  
 Interferon alpha-7 precursor - human  
 N:Alternate names: Interferon alpha-J; LeIF J  
 C:Species: Homo sapiens (man)  
 C:Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 18-Jun-1999  
 C:Accession: A01831; S43717  
 R:Ulrich, A.; Gray, A.; Goeddel, D.V.; Dull, T.J.  
 J. Mol. Biol. 156, 467-486, 1982  
 A:Title: Nucleotide sequence of a portion of human chromosome 9 containing a leukocyte 1  
 A:Reference number: A01831; MUID:83010248  
 A:Accession: A01831  
 A:Molecule type: DNA  
 A:Residues: 1-189 <OUL>  
 A:Cross-references: GB:V00531; NID:q32631; PIDN:CAA23792.1; PID:q32632; DDBJ:J00217  
 A:Note: this interferon is derived from a gene referred to as J by the authors  
 R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: S43717  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: EMBL:X02960; NID:q32665; PIDN:CAA26706.1; PID:q758081  
 C:Genetics:  
 A:Gene: GDB:IFNA7  
 A:Cross-references: GDB:136364; OMIM:147567  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-7 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7% Score 36; DB 1; Length 189;  
 Best Local Similarity 87.5% Pred. No. 4.9;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKYP 8  
 I I I I I I I I

Db 154 LMEKKYSP 161

Search completed: January 15, 2002, 08:40:57  
 Job time: 254 sec